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(21) International Application Number: PCT/US96/18003			(72) Inventors: ENSIGN, Jerald, C.; 1810 North Walnut Street, Madison, WI 53705 (US). BOWEN, David, J.; 5668 Highway A, Oregon, WI 53575 (US). PETELL, James; 1427 Hunters Glen, Zionsville, IN 46077 (US). FATIG, Raymond; 30 Clay Court, Zionsville, IN 46077 (US). SCHOONOVER, Sue; 7142 Marstella, Brownsburg, IN 46112 (US). FFRENCH-CONSTANT, Richard, H.; 1006 University Bay Drive, Madison, WI 53705 (US). ROCHE-LEAU, Thomas, A.; 3100 Buena Vista Street, Madison, WI 53704 (US). BLACKBURN, Michael, B.; 2127 Luann Lane, Madison, WI 53713 (US). HEY, Timothy, D.; 1653 Catalina Way, Zionsville, IN 46077 (US). MERLO, Donald, J.; 11845 Durbin Drive, Carmel, IN 46032 (US). ORR, Gregory, L.; 1028 Saratoga Circle, Indianapolis, IN 46280 (US). ROBERTS, Jean, L.; 26035 State Road 19, Arcadia, IN 46030 (US). STRICKLAND, James, A.; 780 Mt. Zion Road, Lebanon, IN 46052 (US). GUO, Lining; 7 Nelson Circle, Brownsburg, IN 46112 (US). CICHE, Todd, A.; 1609 Chadbourne Avenue, Madison, WI 53705 (US).
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(71) Applicant: WISCONSIN ALUMNI RESEARCH FOUNDATION [US/US]; 614 North Walnut Street, Madison, WI 53707-7365 (US).			
			(74) Agent: SEAY, Nicholas, J.; Quarles & Brady, P.O. Box 2113, Madison, WI 53701-2113 (US).
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(57) Abstract			
Proteins from the genus <i>Photorhabdus</i> are toxic to insects upon exposure. <i>Photorhabdus luminescens</i> (formerly <i>Xenorhabdus luminescens</i>) have been found in mammalian clinical samples and as a bacterial symbiont of entomopathogenic nematodes of genus <i>Heterorhabditis</i> . These protein toxins can be applied to, or genetically engineered into, insect larvae food and plants for insect control.			

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INSECTICIDAL PROTEIN TOXINS FROM *PHOTORHABDUS*

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Field of the Invention

The present invention relates to toxins isolated from bacteria and the use of said toxins as insecticides.

20

Background of the Invention

Many insects are widely regarded as pests to homeowners, to picnickers, to gardeners, and to farmers and others whose
25 investments in agricultural products are often destroyed or diminished as a result of insect damage to field crops. Particularly in areas where the growing season is short, significant insect damage can mean the loss of all profits to growers and a dramatic decrease in crop yield. Scarce supply of
30 particular agricultural products invariably results in higher costs to food processors and, then, to the ultimate consumers of food plants and products derived from those plants.

Preventing insect damage to crops and flowers and eliminating the nuisance of insect pests have typically relied on
35 strong organic pesticides and insecticides with broad toxicities. These synthetic products have come under attack by the general population as being too harsh on the environment and on those exposed to such agents. Similarly in non-agricultural settings, homeowners would be satisfied to have insects avoid their homes
40 or outdoor meals without needing to kill the insects.

The extensive use of chemical insecticides has raised environmental and health concerns for farmers, companies that produce the insecticides, government agencies, public interest groups, and the public in general. The development of less
5 intrusive pest management strategies has been spurred along both by societal concern for the environment and by the development of biological tools which exploit mechanisms of insect management. Biological control agents present a promising alternative to chemical insecticides.

10 Organisms at every evolutionary development level have devised means to enhance their own success and survival. The use of biological molecules as tools of defense and aggression is known throughout the animal and plant kingdoms. In addition, the relatively new tools of the genetic engineer allow modifications
15 to biological insecticides to accomplish particular solutions to particular problems.

One such agent, *Bacillus thuringiensis* (Bt), is an effective insecticidal agent, and is widely commercially used as such. In fact, the insecticidal agent of the Bt bacterium is a protein
20 which has such limited toxicity, it can be used on human food crops on the day of harvest. To non-targeted organisms, the Bt toxin is a digestible non-toxic protein.

Another known class of biological insect control agents are certain genera of nematodes known to be vectors of transmission
25 for insect-killing bacterial symbionts. Nematodes containing insecticidal bacteria invade insect larvae. The bacteria then kill the larvae. The nematodes reproduce in the larval cadaver. The nematode progeny then eat the cadaver from within. The bacteria-containing nematode progeny thus produced can then
30 invade additional larvae.

In the past, insecticidal nematodes in the *Steinernema* and *Heterorhabditis* genera were used as insect control agents. Apparently, each genus of nematode hosts a particular species of bacterium. In nematodes of the *Heterorhabditis* genus, the
35 symbiotic bacterium is *Photorhabdus luminescens*.

Although these nematodes are effective insect control agents, it is presently difficult, expensive, and inefficient to produce, maintain, and distribute nematodes for insect control.

It has been known in the art that one may isolate an
40 insecticidal toxin from *Photorhabdus luminescens* that has

activity only when injected into Lepidopteran and Coleopteran insect larvae. This has made it impossible to effectively exploit the insecticidal properties of the nematode or its bacterial symbiont. What would be useful would be a more
5 practical, less labor-intensive wide-area delivery method of an insecticidal toxin which would retain its biological properties after delivery. It would be quite desirable to discover toxins with oral activity produced by the genus *Photorhabdus*. The isolation and use of these toxins are desirable due to efficacious
10 reasons. Until applicants' discoveries, these toxins had not been isolated or characterized.

Summary of the Invention

15 The native toxins are protein complexes that are produced and secreted by growing bacteria cells of the genus *Photorhabdus*, of interest are the proteins produced by the species *Photorhabdus luminescens*. The protein complexes, with a molecular size of approximately 1,000 kDa, can be separated by SDS-PAGE gel
20 analysis into numerous component proteins. The toxins contain no hemolysin, lipase, type C phospholipase, or nuclease activities. The toxins exhibit significant toxicity upon exposure administration to a number of insects.

The present invention provides an easily administered
25 insecticidal protein as well as the expression of toxin in a heterologous system.

The present invention also provides a method for delivering insecticidal toxins that are functional active and effective against many orders of insects.

30 Objects, advantages, and features of the present invention will become apparent from the following specification.

Brief Description of the Drawings

35 Fig. 1 is an illustration of a match of cloned DNA isolates used as a part of sequence genes for the toxin of the present invention.

Fig. 2 is a map of three plasmids used in the sequencing process.

Fig. 3 is a map illustrating the inter-relationship of several partial DNA fragments.

Fig. 4 is an illustration of a homology analysis between the protein sequences of TcbAii and TcaBii proteins.

5 Fig. 5 is a phenogram of *Photobhabdus* strains. Relationship of *Photobhabdus* Strains was defined by rep-PCR.

The upper axis of Fig. 5 measures the percentage similarity of strains based on scoring of rep-PCR products (i.e., 0.0 [no similarity] to 1.0 [100% similarity]). At the right axis, the numbers and letters indicate the various strains tested; 14=W-14, Hm=Hm, H9=H9, 7=WX-7, 1=WX-1, 2=WX-2, 88=HP88, NC-1=NC-1, 4=WX-4, 9=WX-9, 8=WX-8, 10=WX-10, WIR=WIR, 3=WX-3, 11=WX-11, 5=WX-5, 6=WX-6, 12=WX-12, x14=WX-14, 15=WX-15, Hb=Hb, B2=B2, 48 through 52=ATCC 43948 through ATCC 43952. Vertical lines separating horizontal lines indicate the degree of relatedness (as read from the extrapolated intersection of the vertical line with the upper axis) between strains or groups of strains at the base of the horizontal lines (e.g., strain W-14 is approximately 60% similar to strains H9 and Hm).

20 Fig. 6 is an illustration of the genomic maps of the W-14 Strain.

Detailed Description of the Invention

25 The present inventions are directed to the discovery of a unique class of insecticidal protein toxins from the genus *Photobhabdus* that have oral toxicity against insects. A unique feature of *Photobhabdus* is its bioluminescence. *Photobhabdus* may be isolated from a variety of sources. One such source is nematodes, more particularly nematodes of the genus *Heterorhabditis*. Another such source is from human clinical samples from wounds, see Farmer et al. 1989 J. Clin. Microbiol. 27 pp. 1594-1600. These saprophytic strains are deposited in the American Type Culture Collection (Rockville, MD) ATCC #s 43948, 43949, 43950, 43951, and 43952, and are incorporated herein by reference. It is possible that other sources could harbor *Photobhabdus* bacteria that produce insecticidal toxins. Such sources in the environment could be either terrestrial or aquatic based.

The genus *Photorhabdus* is taxonomically defined as a member of the Family *Enterobacteriaceae*, although it has certain traits atypical of this family. For example, strains of this genus are nitrate reduction negative, yellow and red pigment producing and bioluminescent. This latter trait is otherwise unknown within the *Enterobacteriaceae*. *Photorhabdus* has only recently been described as a genus separate from the *Xenorhabdus* (Boemare et al., 1993 Int. J. Syst. Bacteriol. 43, 249-255). This differentiation is based on DNA-DNA hybridization studies, phenotypic differences (e.g., presence (*Photorhabdus*) or absence (*Xenorhabdus*) of catalase and bioluminescence) and the Family of the nematode host (*Xenorhabdus*; *Steinernematidae*, *Photorhabdus*; *Heterorhabditidae*). Comparative, cellular fatty-acid analyses (Janse et al. 1990, Lett. Appl. Microbiol 10, 131-135; Suzuki et al. 1990, J. Gen. Appl. Microbiol., 36, 393-401) support the separation of *Photorhabdus* from *Xenorhabdus*.

In order to establish that the strain collection disclosed herein was comprised of *Photorhabdus* strains, the strains were characterized based on recognized traits which define *Photorhabdus* and differentiate it from other *Enterobacteriaceae* and *Xenorhabdus* species. (Farmer, 1984 Bergey's Manual of Systemic Bacteriology Vol. 1 pp.510-511; Akhurst and Boemare 1988, J. Gen. Microbiol. 134 pp.1835-1845; Boemare et al. 1993 Int. J. Syst. Bacteriol. 43 pp.249-255, which are incorporated herein by reference). The traits studied were the following: gram stain negative rods, organism size, colony pigmentation, inclusion bodies, presence of catalase, ability to reduce nitrate, bioluminescence, dye uptake, gelatin hydrolysis, growth on selective media, growth temperature, survival under anerobic conditions and motility. Fatty acid analysis was used to confirm that the strains herein all belong to the single genus *Photorhabdus*.

Currently, the bacterial genus *Photorhabdus* is comprised of a single defined species, *Photorhabdus luminescens* (ATCC Type strain #29999, Poinar et al., 1977, Nematologica 23, 97-102). A variety of related strains have been described in the literature (e.g. Akhurst et al. 1988 J. Gen. Microbiol., 134, 1835-1845; Boemare et al. 1993 Int. J. Syst. Bacteriol. 43 pp. 249-255; Putz et al. 1990, Appl. Environ. Microbiol., 56, 181-186). Numerous

Photorhabdus strains have been characterized herein. Such strains are listed in Table 18 in the Examples. Because there is currently only one species (*luminescens*) defined within the genus *Photorhabdus*, the *luminescens* species traits were used to
5 characterize the strains herein. As can be seen in Fig. 5, these strains are quite diverse. It is not unforeseen that in the future there may be other *Photorhabdus* species that will have some of the attributes of the *luminescens* species as well as some different characteristics that are presently not defined as a
10 trait of *Photorhabdus luminescens*. However, the scope of the invention herein is to any *Photorhabdus* species or strains which produce proteins that have functional activity as insect control agents, regardless of other traits and characteristics.

Furthermore, as is demonstrated herein, the bacteria of the
15 genus *Photorhabdus* produce proteins that have functional activity as defined herein. Of particular interest are proteins produced by the species *Photorhabdus luminescens*. The inventions herein should in no way be limited to the strains which are disclosed herein. These strains illustrate for the first time that
20 proteins produced by diverse isolates of *Photorhabdus* are toxic upon exposure to insects. Thus, included within the inventions described herein are the strains specified herein and any mutants thereof, as well as any strains or species of the genus
Photorhabdus that have the functional activity described herein.

25 There are several terms that are used herein that have a particular meaning and are as follows:

By "functional activity" it is meant herein that the protein toxins function as insect control agents in that the proteins are
30 orally active, or have a toxic effect, or are able to disrupt or deter feeding, which may or may not cause death of the insect. When an insect comes into contact with an effective amount of toxin delivered via transgenic plant expression, formulated protein compositions(s), sprayable protein composition(s), a bait
35 matrix or other delivery system, the results are typically death of the insect, or the insects do not feed upon the source which makes the toxins available to the insects.

The protein toxins discussed herein are typically referred to as "insecticides". By insecticides it is meant herein that the protein toxins have a "functional activity" as further defined herein and are used as insect control agents.

5

By the use of the term "oligonucleotides" it is meant a macromolecule consisting of a short chain of nucleotides of either RNA or DNA. Such length could be at least one nucleotide, but typically are in the range of about 10 to about 12

10 nucleotides. The determination of the length of the oligonucleotide is well within the skill of an artisan and should not be a limitation herein. Therefore, oligonucleotides may be less than 10 or greater than 12.

15 By the use of the term "toxic" or "toxicity" as used herein it is meant that the toxins produced by *Photorhabdus* have "functional activity" as defined herein.

By the use of the term "genetic material" herein, it is meant to
20 include all genes, nucleic acid, DNA and RNA.

Fermentation broths from selected strains reported in Table 18 were used to determine the following: breadth of insecticidal toxin production by the *Photorhabdus* genus, the
25 insecticidal spectrum of these toxins, and to provide source material to purify the toxin complexes. The strains characterized herein have been shown to have oral toxicity against a variety of insect orders. Such insect orders include but are not limited to *Coleoptera*, *Homoptera*, *Lepidoptera*,
30 *Diptera*, *Acarina*, *Hymenoptera* and *Dictyoptera*.

As with other bacterial toxins, the rate of mutation of the bacteria in a population causes many related toxins slightly different in sequence to exist. Toxins of interest here are
35 those which produce protein complexes toxic to a variety of insects upon exposure, as described herein. Preferably, the toxins are active against *Lepidoptera*, *Coleoptera*, *Homoptera*, *Diptera*, *Hymenoptera*, *Dictyoptera* and *Acarina*. The inventions herein are intended to capture the protein toxins homologous to
40 protein toxins produced by the strains herein and any derivative

5 By the use of the term "*Photorhabdus* toxin" it is meant any
protein produced by a *Photorhabdus* microorganism strain
which has functional activity against insects, where the
Photorhabdus toxin could be formulated as a sprayable
composition, expressed by a transgenic plant, formulated as
10 a bait matrix, delivered via a Baculovirus, or delivered by
any other applicable host or delivery system.

strains thereof, as well as any protein toxins produced by *Photorhabdus*. These homologous proteins may differ in sequence, but do not differ in function from those toxins described herein. Homologous toxins are meant to include protein complexes of
5 between 300 kDa to 2,000 kDa and are comprised of at least two (2) subunits, where a subunit is a peptide which may or may not be the same as the other subunit. Various protein subunits have been identified and are taught in the Examples herein. Typically, the protein subunits are between about 18 kDa to about
10 230 kDa; between about 160 kDa to about 230 kDa; 100 kDa to 160 kDa; about 80 kDa to about 100 kDa; and about 50 kDa to about 80 kDa.

As discussed above, some *Photorhabdus* strains can be isolated from nematodes. Some nematodes, elongated cylindrical
15 parasitic worms of the phylum *Nematoda*, have evolved an ability to exploit insect larvae as a favored growth environment. The insect larvae provide a source of food for growing nematodes and an environment in which to reproduce. One dramatic effect that follows invasion of larvae by certain nematodes is larval death.
20 Larval death results from the presence of, in certain nematodes, bacteria that produce an insecticidal toxin which arrests larval growth and inhibits feeding activity.

Interestingly, it appears that each genus of insect parasitic nematode hosts a particular species of bacterium,
25 uniquely adapted for symbiotic growth with that nematode. In the interim since this research was initiated, the name of the bacterial genus *Xenorhabdus* was reclassified into the *Xenorhabdus* and the *Photorhabdus*. Bacteria of the genus *Photorhabdus* are characterized as being symbionts of *Heterorhabditus* nematodes
30 while *Xenorhabdus* species are symbionts of the *Steinernema* species. This change in nomenclature is reflected in this specification, but in no way should a change in nomenclature alter the scope of the inventions described herein.

The peptides and genes that are disclosed herein are named
35 according to the guidelines recently published in the Journal of Bacteriology "Instructions to Authors" p. i-xii (Jan. 1996), which is incorporated herein by reference. The following peptides and genes were isolated from *Photorhabdus* strain W-14.

Peptide / Gene Nomenclature
Toxin complex (Tc)

5	Peptide Name	Gene Name	Patent Sequence ID#
	<u>tca genomic region</u>		
	TcaA	tcaA	12
	TcaAiii	tcaA	4
10	TcaBi	tcaB	3 (19, 20)
	TcaBii	tcaB	5
	TcaC	tcaC	2
	<u>tcb genomic region</u>		
15	TcbA	tcbA	16
	TcbAi	tcbA	(pro-peptide)
	TcbAii	tcbA	1 (21, 22, 23, 24)
	TcbAiii	tcbA	40
20	<u>tcc genomic region</u>		
	TccA	tccA	8
	TccB	tccB	7
	<u>tcd genomic region</u>		
25	TcdAi	tcdA	(pro-peptide)
	TcdAii	tcdA	13, (38, 39 17, 18)
	TcdAiii	tcdA	41, (42, 43)
30	TcdB	tcdB	14

(bracket sequence indicates internal amino acid sequence obtained by tryptic digests)

35 The sequences listed above are grouped by genomic region.
The *tcbA* gene was expressed in *E. coli* as two protein fragments
TcbA and TcbAiii as illustrated in the Examples. It may be
beneficial to have proteolytic clippage of some sequences to
obtain the higher activity of the toxins for commercial
40 transgenic applications.

 The toxins described herein are quite unique in that the
toxins have functional activity, which is key to developing an
insect management strategy. In developing an insect management
45 strategy, it is possible to delay or circumvent the protein
degradation process by injecting a protein directly into an
organism, avoiding its digestive tract. In such cases, the
protein administered to the organism will retain its function
until it is denatured, non-specifically degraded, or eliminated
50 by the immune system in higher organisms. Injection into insects

of an insecticidal toxin has potential application only in the laboratory, and then only on large insects which are easily injected. The observation that the insecticidal protein toxins herein described exhibits their toxic activity after oral
5 ingestion or contact with the toxins permits the development of an insect management plan based solely on the ability to incorporate the protein toxins into the insect diet. Such a plan could result in the production of insect baits.

The *Photorhabdus* toxins may be administered to insects in a
10 purified form. The toxins may also be delivered in amounts from about 1 to about 100 mg / liter of broth. This may vary upon formulation condition, conditions of the inoculum source, techniques for isolation of the toxin, and the like. The toxins may be administered as an exudate secretion or cellular protein
15 originally expressed in a heterologous prokaryotic or eukaryotic host. Bacteria are typically the hosts in which proteins are expressed. Eukaryotic hosts could include but are not limited to plants, insects and yeast. Alternatively, the toxins may be produced in bacteria or transgenic plants in the field or in the
20 insect by a baculovirus vector. Typically the toxins will be introduced to the insect by incorporating one or more of the toxins into the insects' feed.

Complete lethality to feeding insects is useful but is not required to achieve useful toxicity. If the insects avoid the
25 toxin or cease feeding, that avoidance will be useful in some applications, even if the effects are sublethal. For example, if insect resistant transgenic crop plants are desired, a reluctance of insects to feed on the plants is as useful as lethal toxicity to the insects since the ultimate objective is protection of the
30 plants rather than killing the insect.

There are many other ways in which toxins can be incorporated into an insect's diet. As an example, it is possible to adulterate the larval food source with the toxic protein by spraying the food with a protein solution, as
35 disclosed herein. Alternatively, the purified protein could be genetically engineered into an otherwise harmless bacterium, which could then be grown in culture, and either applied to the food source or allowed to reside in the soil in an area in which insect eradication was desirable. Also, the protein could be
40 genetically engineered directly into an insect food source. For

be transformed during dedifferentiation using appropriate techniques within the skill of an artisan.

Another variable is the choice of a selectable marker. The preference for a particular marker is at the discretion of the artisan, but any of the following selectable markers may be used along with any other gene not listed herein which could function as a selectable marker. Such selectable markers include but are not limited to aminoglycoside phosphotransferase gene of transposon Tn5 (Aph II) which encodes resistance to the antibiotics kanamycin, neomycin and G418, as well as those genes which code for resistance or tolerance to glyphosate; hygromycin; methotrexate; phosphinothricin (bialophos); imidazolinones, sulfonylureas and triazolopyrimidine herbicides, such as chlorosulfuron; bromoxynil, dalapon and the like.

In addition to a selectable marker, it may be desirable to use a reporter gene. In some instances a reporter gene may be used without a selectable marker. Reporter genes are genes which are typically not present or expressed in the recipient organism or tissue. The reporter gene typically encodes for a protein which provides for some phenotypic change or enzymatic property. Examples of such genes are provided in K. Weising et al. Ann. Rev. Genetics, 22, 421 (1988), which is incorporated herein by reference. A preferred reporter gene is the glucuronidase (GUS) gene.

Regardless of transformation technique, the gene is preferably incorporated into a gene transfer vector adapted to express the *Photorhabdus* toxins in the plant cell by including in the vector a plant promoter. In addition to plant promoters, promoters from a variety of sources can be used efficiently in plant cells to express foreign genes. For example, promoters of bacterial origin, such as the octopine synthase promoter, the nopaline synthase promoter, the mannopine synthase promoter; promoters of viral origin, such as the cauliflower mosaic virus (35S and 19S) and the like may be used. Plant promoters include, but are not limited to ribulose-1,6-bisphosphate (RUBP) carboxylase small subunit (ssu), beta-conglycinin promoter, phaseolin promoter, ADH promoter, heat-shock promoters and tissue specific promoters. Promoters may also contain certain enhancer sequence elements that may improve the transcription efficiency. Typical enhancers include but are not limited to Adh-intron 1 and

Adh-intron 6. Constitutive promoters may be used. Constitutive promoters direct continuous gene expression in all cells types and at all times (e.g., actin, ubiquitin, CaMV 35S). Tissue specific promoters are responsible for gene expression in
5 specific cell or tissue types, such as the leaves or seeds (e.g., zein, oleosin, napin, ACP) and these promoters may also be used. Promoters may also be are active during a certain stage of the plants' development as well as active in plant tissues and organs. Examples of such promoters include but are not limited
10 to pollen-specific, embryo specific, corn silk specific, cotton fiber specific, root specific, seed endosperm specific promoters and the like.

Under certain circumstances it may be desirable to use an inducible promoter. An inducible promoter is responsible for
15 expression of genes in response to a specific signal, such as: physical stimulus (heat shock genes); light (RUBP carboxylase); hormone (Em); metabolites; and stress. Other desirable transcription and translation elements that function in plants may be used. Numerous plant-specific gene transfer vectors are
20 known to the art.

In addition, it is known that to obtain high expression of bacterial genes in plants it is preferred to reengineer the bacterial genes so that they are more efficiently expressed in the cytoplasm of plants. Maize is one such plant where it is
25 preferred to reengineer the bacterial gene(s) prior to transformation to increase the expression level of the toxin in the plant. One reason for the reengineering is the very low G+C content of the native bacterial gene(s) (and consequent skewing towards high A+T content). This results in the generation of
30 sequences mimicking or duplicating plant gene control sequences that are known to be highly A+T rich. The presence of some A+T-rich sequences within the DNA of the gene(s) introduced into plants (e.g., TATA box regions normally found in gene promoters) may result in aberrant transcription of the gene(s). On the
35 other hand, the presence of other regulatory sequences residing in the transcribed mRNA (e.g., polyadenylation signal sequences (AAUAAA), or sequences complementary to small nuclear RNAs involved in pre-mRNA splicing) may lead to RNA instability. Therefore, one goal in the design of reengineered bacterial

gene(s), more preferably referred to as plant optimized gene(s), is to generate a DNA sequence having a higher G+C content, and preferably one close to that of plant genes coding for metabolic enzymes. Another goal in the design of the plant optimized gene(s) is to generate a DNA sequence that not only has a higher G+C content, but by modifying the sequence changes, should be made so as to not hinder translation.

An example of a plant that has a high G+C content is maize. The table below illustrates how high the G+C content is in maize. As in maize, it is thought that G+C content in other plants is also high.

Table 1
Compilation of G+C contents of protein coding regions
of maize genes

Protein Class ^a	Range %G+C	Mean %G+C ^b
Metabolic Enzymes (40)	44.4-75.3	59.0 (8.0)
Storage Proteins		
Group I (23)	46.0-51.9	48.1 (1.3)
Group II (13)	60.4-74.3	67.5 (3.2)
Group I + II (36)	46.0-74.3	55.1 (9.6) ^c
Structural Proteins (18)	48.6-70.5	63.6 (6.7)
Regulatory Proteins (5)	57.2-68.9	62.0 (4.9)
Uncharacterized Proteins (9)	41.5-70.3	64.3 (7.2)
All Proteins (108)	44.4-75.3	60.8 (5.2)

^a Number of genes in class given in parentheses.

^b Standard deviations given in parentheses.

^c Combined groups mean ignored in calculation of overall mean.

For the data in Table 1, coding regions of the genes were extracted from GenBank (Release 71) entries, and base compositions were calculated using the MacVector™ program (IBI, New Haven, CT). Intron sequences were ignored in the

calculations. Group I and II storage protein gene sequences were distinguished by their marked difference in base composition.

Due to the plasticity afforded by the redundancy of the genetic code (i.e., some amino acids are specified by more than one codon), evolution of the genomes of different organisms or classes of organisms has resulted in differential usage of redundant codons. This "codon bias" is reflected in the mean base composition of protein coding regions. For example, organisms with relatively low G+C contents utilize codons having A or T in the third position of redundant codons, whereas those having higher G+C contents utilize codons having G or C in the third position. It is thought that the presence of "minor" codons within a gene's mRNA may reduce the absolute translation rate of that mRNA, especially when the relative abundance of the charged tRNA corresponding to the minor codon is low. An extension of this is that the diminution of translation rate by individual minor codons would be at least additive for multiple minor codons. Therefore, mRNAs having high relative contents of minor codons would have correspondingly low translation rates. This rate would be reflected by the synthesis of low levels of the encoded protein.

In order to reengineer the bacterial gene(s), the codon bias of the plant is determined. The codon bias is the statistical codon distribution that the plant uses for coding its proteins. After determining the bias, the percent frequency of the codons in the gene(s) of interest is determined. The primary codons preferred by the plant should be determined as well as the second and third choice of preferred codons. The amino acid sequence of the protein of interest is reverse translated so that the resulting nucleic acid sequence codes for the same protein as the native bacterial gene, but the resulting nucleic acid sequence corresponds to the first preferred codons of the desired plant. The new sequence is analyzed for restriction enzyme sites that might have been created by the modification. The identified sites are further modified by replacing the codons with second or third choice preferred codons. Other sites in the sequence which could affect the transcription or translation of the gene of interest are the exon:intron 5' or 3' junctions, poly A addition signals, or RNA polymerase termination signals. The sequence is

further analyzed and modified to reduce the frequency of TA or GC doublets. In addition to the doublets, G or C sequence blocks that have more than about four residues that are the same can affect transcription of the sequence. Therefore, these blocks
5 are also modified by replacing the codons of first or second choice, etc. with the next preferred codon of choice. It is preferred that the plant optimized gene(s) contains about 63% of first choice codons, between about 22% to about 37% second choice codons, and between 15% and 0% third choice codons, wherein the
10 total percentage is 100%. Most preferred the plant optimized gene(s) contain about 63% of first choice codons, at least about 22% second choice codons, about 7.5% third choice codons, and about 7.5% fourth choice codons, wherein the total percentage is 100%. The method described above enables one skilled in the art
15 to modify gene(s) that are foreign to a particular plant so that the genes are optimally expressed in plants. The method is further illustrated in pending provisional application U.S. 60/005,405 filed on October 13, 1995, which is incorporated herein by reference.

20 Thus, in order to design plant optimized gene(s) the amino acid sequence of the toxins are reverse translated into a DNA sequence, utilizing a nonredundant genetic code established from a codon bias table compiled for the gene DNA sequence for the particular plant being transformed. The resulting DNA sequence,
25 which is completely homogeneous in codon usage, is further modified to establish a DNA sequence that, besides having a higher degree of codon diversity, also contains strategically placed restriction enzyme recognition sites, desirable base composition, and a lack of sequences that might interfere with
30 transcription of the gene, or translation of the product mRNA.

It is theorized that bacterial genes may be more easily expressed in plants if the bacterial genes are expressed in the plastids. Thus, it may be possible to express bacterial genes in plants, without optimizing the genes for plant expression, and
35 obtain high express of the protein. See U.S. Patent Nos. 4,762,785; 5,451,513 and 5,545,817, which are incorporated herein by reference.

One of the issues regarding commercial exploiting transgenic plants is resistance management. This is of particular concern with *Bacillus thuringiensis* toxins. There are numerous companies commercially exploiting *Bacillus thuringiensis* and there has been
5 much concern about *Bt* toxins becoming resistant. One strategy for insect resistant management would be to combine the toxins produced by *Photorhabdus* with toxins such as *Bt*, vegetative insect proteins (Ciba Geigy) or other toxins. The combinations could be formulated for a sprayable application or could be
10 molecular combinations. Plants could be transformed with *Photorhabdus* genes that produce insect toxins and other insect toxin genes such as *Bt* as with other insect toxin genes such as *Bt*.

European Patent Application 0400246A1 describes
15 transformation of 2 *Bt* in a plant, which could be any 2 genes. Another way to produce a transgenic plant that contains more than one insect resistant gene would be to produce two plants, with each plant containing an insect resistant gene. These plants would be backcrossed using traditional plant breeding techniques
20 to produce a plant containing more than one insect resistant gene.

In addition to producing a transformed plant containing plant optimized gene(s), there are other delivery systems where it may be desirable to reengineer the bacterial gene(s). Along
25 the same lines, a genetically engineered, easily isolated protein toxin fusing together both a molecule attractive to insects as a food source and the insecticidal activity of the toxin may be engineered and expressed in bacteria or in eukaryotic cells using standard, well-known techniques. After purification in the
30 laboratory such a toxic agent with "built-in" bait could be packaged inside standard insect trap housings.

Another delivery scheme is the incorporation of the genetic material of toxins into a baculovirus vector. Baculoviruses infect particular insect hosts, including those desirably
35 targeted with the *Photorhabdus* toxins. Infectious baculovirus harboring an expression construct for the *Photorhabdus* toxins could be introduced into areas of insect infestation to thereby intoxicate or poison infected insects.

Transfer of the insecticidal properties requires nucleic acid sequences encoding the coding the amino acid sequences for the *Photorhabdus* toxins integrated into a protein expression vector appropriate to the host in which the vector will reside.

5 One way to obtain a nucleic acid sequence encoding a protein with insecticidal properties is to isolate the native genetic material which produces the toxins from *Photorhabdus*, using information deduced from the toxin's amino acid sequence, large portions of which are set forth below. As described below, methods of

10 purifying the proteins responsible for toxin activity are also disclosed.

Using N-terminal amino acid sequence data, such as set forth below, one can construct oligonucleotides complementary to all, or a section of, the DNA bases that encode the first amino acids

15 of the toxin. These oligonucleotides can be radiolabeled and used as molecular probes to isolate the genetic material from a genomic genetic library built from genetic material isolated from strains of *Photorhabdus*. The genetic library can be cloned in plasmid, cosmid, phage or phagemid vectors. The library could be

20 transformed into *Escherichia coli* and screened for toxin production by the transformed cells using antibodies raised against the toxin or direct assays for insect toxicity.

This approach requires the production of a battery of oligonucleotides, since the degenerate genetic code allows an

25 amino acid to be encoded in the DNA by any of several three-nucleotide combinations. For example, the amino acid arginine can be encoded by nucleic acid triplets CGA, CGC, CGG, CGT, AGA, and AGG. Since one cannot predict which triplet is used at those positions in the toxin gene, one must prepare oligonucleotides

30 with each potential triplet represented. More than one DNA molecule corresponding to a protein subunit may be necessary to construct a sufficient number of oligonucleotide probes to recover all of the protein subunits necessary to achieve oral toxicity.

35 From the amino acid sequence of the purified protein, genetic materials responsible for the production of toxins can readily be isolated and cloned, in whole or in part, into an expression vector using any of several techniques well-known to one skilled in the art of molecular biology. A typical

40 expression vector is a DNA plasmid, though other transfer means

including, but not limited to, cosmids, phagemids and phage are also envisioned. In addition to features required or desired for plasmid replication, such as an origin of replication and antibiotic resistance or other form of a selectable marker such as the *bar* gene of *Streptomyces hygrosopicus* or viridochromogenes, protein expression vectors normally additionally require an expression cassette which incorporates the cis-acting sequences necessary for transcription and translation of the gene of interest. The cis-acting sequences required for expression in prokaryotes differ from those required in eukaryotes and plants.

A eukaryotic expression cassette requires a transcriptional promoter upstream (5') to the gene of interest, a transcriptional termination region such as a poly-A addition site, and a ribosome binding site upstream of the gene of interest's first codon. In bacterial cells, a useful transcriptional promoter that could be included in the vector is the T7 RNA Polymerase-binding promoter. Promoters, as previously described herein, are known to efficiently promote transcription of mRNA. Also upstream from the gene of interest the vector may include a nucleotide sequence encoding a signal sequence known to direct a covalently linked protein to a particular compartment of the host cells such as the cell surface.

Insect viruses, or baculoviruses, are known to infect and adversely affect certain insects. The affect of the viruses on insects is slow, and viruses do not stop the feeding of insects. Thus viruses are not viewed as being useful as insect pest control agents. Combining the *Photobacterium* toxins genes into a baculovirus vector could provide an efficient way of transmitting the toxins while increasing the lethality of the virus. In addition, since different baculoviruses are specific to different insects, it may be possible to use a particular toxin to selectively target particularly damaging insect pests. A particularly useful vector for the toxins genes is the nuclear polyhedrosis virus. Transfer vectors using this virus have been described and are now the vectors of choice for transferring foreign genes into insects. The virus-toxin gene recombinant may be constructed in an orally transmissible form. Baculoviruses normally infect insect victims through the mid-gut intestinal mucosa. The toxin gene inserted behind a strong viral coat

protein promoter would be expressed and should rapidly kill the infected insect.

In addition to an insect virus or baculovirus or transgenic plant delivery system for the protein toxins of the present invention, the proteins may be encapsulated using *Bacillus thuringiensis* encapsulation technology such as but not limited to U.S. Patent Nos. 4,695,455; 4,695,462; 4,861,595 which are all incorporated herein by reference. Another delivery system for the protein toxins of the present invention is formulation of the protein into a bait matrix, which could then be used in above and below ground insect bait stations. Examples of such technology include but are not limited to PCT Patent Application WO 93/23998, which is incorporated herein by reference.

As is described above, it might become necessary to modify the sequence encoding the protein when expressing it in a non-native host, since the codon preferences of other hosts may differ from that of *Photobacterium*. In such a case, translation may be quite inefficient in a new host unless compensating modifications to the coding sequence are made. Additionally, modifications to the amino acid sequence might be desirable to avoid inhibitory cross-reactivity with proteins of the new host, or to refine the insecticidal properties of the protein in the new host. A genetically modified toxin gene might encode a toxin exhibiting, for example, enhanced or reduced toxicity, altered insect resistance development, altered stability, or modified target species specificity.

In addition to the *Photobacterium* genes encoding the toxins, the scope of the present invention is intended to include related nucleic acid sequences which encode amino acid biopolymers homologous to the toxin proteins and which retain the toxic effect of the *Photobacterium* proteins in insect species after oral ingestion.

For instance, the toxins used in the present invention seem to first inhibit larval feeding before death ensues. By manipulating the nucleic acid sequence of *Photobacterium* toxins or its controlling sequences, genetic engineers placing the toxin gene into plants could modulate its potency or its mode of action to, for example, keep the eating-inhibitory activity while eliminating the absolute toxicity to the larvae. This change could permit the transformed plant to survive until harvest

without having the unnecessarily dramatic effect on the ecosystem of wiping out all target insects. All such modifications of the gene encoding the toxin, or of the protein encoded by the gene, are envisioned to fall within the scope of the present invention.

5 Other envisioned modifications of the nucleic acid include the addition of targeting sequences to direct the toxin to particular parts of the insect larvae for improving its efficiency.

10 Strains ATCC 55397, 43948, 43949, 43950, 43951, 43952 have been deposited in the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD 20852 USA. Amino acid and nucleotide sequence data for the W-14 native toxin (ATCC 55397) is presented below. Isolation of the genomic DNA for the toxins from the bacterial hosts is also exemplified herein.

15 Standard and molecular biology techniques were followed and taught in the specification herein. Additional information may be found in Sambrook, J., Fritsch, E. F., and Maniatis, T. (1989), Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, which is incorporated herein by reference.

20

The following abbreviations are used throughout the Examples: Tris = tris (hydroxymethyl) amino methane; SDS = sodium dodecyl sulfate; EDTA = ethylenediaminetetraacetic acid, IPTG = isopropylthio-B-galactoside, X-gal = 5-bromo-4-chloro-3-indoyl-B-D-galactoside, CTAB = cetyltrimethylammonium bromide; kbp = 25 kilobase pairs; dATP, dCTP, dGTP, dTTP, I = 2'-deoxynucleoside 5'-triphosphates of adenine, cytosine, guanine, thymine, and inosine, respectively; ATP = adenosine 5' triphosphate.

30

Example 1

Purification of toxin from *P. luminescens* and Demonstration of toxicity after oral delivery of purified toxin

35 The insecticidal protein toxin of the present invention was purified from *P. luminescens* strain W-14, ATCC Accession Number 55397. Stock cultures of *P. luminescens* were maintained on petri dishes containing 2% Proteose Peptone No. 3 (i.e., PP3, Difco Laboratories, Detroit MI) in 1.5% agar, incubated at 25°C and transferred weekly. Colonies of the primary form of the bacteria 40 were inoculated into 200 ml of PP3 broth supplemented with 0.5%

polyoxyethylene sorbitan mono-stearate (Tween 60, Sigma Chemical Company, St. Louis MO) in a one liter flask. The broth cultures were grown for 72 hours at 30°C on a rotary shaker. The toxin proteins can be recovered from cultures grown in the presence or
5 absence of Tween; however, the absence of Tween can affect the form of the bacteria grown and the profile of proteins produced by the bacteria. In the absence of Tween, a variant shift occurs insofar as the molecular weight of at least one identified toxin subunit shifts from about 200 kDa to about 185 kDa.

10 The 72 hour cultures were centrifuged at 10,000 x g for 30 minutes to remove cells and debris. The supernatant fraction that contained the insecticidal activity was decanted and brought to 50 mM K₂HPO₄ by adding an appropriate volume of 1.0 M K₂HPO₄. The pH was adjusted to 8.6 by adding potassium hydroxide. This
15 supernatant fraction was then mixed with DEAE-Sephacel (Pharmacia LKB Biotechnology) which had been equilibrated with 50 mM K₂HPO₄. The toxic activity was adsorbed to the DEAE resin. This mixture was then poured into a 2.6 x 40 cm column and washed with 50 mM K₂HPO₄ at room temperature at a flow rate of 30 ml/hr until the
20 effluent reached a steady baseline UV absorbance at 280 nm. The column was then washed with 150 mM KCl until the effluent again reached a steady 280 nm baseline. Finally the column was washed with 300 mM KCl and fractions were collected.

Fractions containing the toxin were pooled and filter
25 sterilized using a 0.2 micron pore membrane filter. The toxin was then concentrated and equilibrated to 100 mM KPO₄, pH 6.9, using an ultrafiltration membrane with a molecular weight cutoff of 100 kDa at 4°C (Centriprep 100, Amicon Division-W.R. Grace and Company). A 3 ml sample of the toxin concentrate was applied to
30 the top of a 2.6 x 95 cm Sephacryl S-400 HR gel filtration column (Pharmacia LKB Biotechnology). The eluent buffer was 100 mM KPO₄, pH 6.9, which was run at a flow rate of 17 ml/hr, at 4°C. The effluent was monitored at 280 nm.

Fractions were collected and tested for toxic activity.
35 Toxicity of chromatographic fractions was examined in a biological assay using *Manduca sexta* larvae. Fractions were either applied directly onto the insect diet (Gypsy moth wheat germ diet, ICN Biochemicals Division - ICN Biomedicals, Inc.) or administered by intrahemocoelic injection of a 5 µl sample through
40 the first proleg of 4th or 5th instar larva using a 30 gauge

needle. The weight of each larva within a treatment group was recorded at 24 hour intervals. Toxicity was presumed if the insect ceased feeding and died within several days of consuming treated insect diet or if death occurred within 24 hours after
5 injection of a fraction.

The toxic fractions were pooled and concentrated using the Centriprep-100 and were then analyzed by HPLC using a 7.5 mm x 60 cm TSK-GEL G-4000 SW gel permeation column with 100 mM potassium phosphate, pH 6.9 eluent buffer running at 0.4 ml/min. This
10 analysis revealed the toxin protein to be contained within a single sharp peak that eluted from the column with a retention time of approximately 33.6 minutes. This retention time corresponded to an estimated molecular weight of 1,000 kDa. Peak fractions were collected for further purification while fractions
15 not containing this protein were discarded. The peak eluted from the HPLC absorbs UV light at 218 and 280 nm but did not absorb at 405 nm. Absorbance at 405 nm was shown to be an attribute of xenorhabdin antibiotic compounds.

Electrophoresis of the pooled peak fractions in a non-
20 denaturing agarose gel (Metaphor Agarose, FMC BioProducts) showed that two protein complexes are present in the peak. The peak material, buffered in 50 mM Tris-HCl, pH 7.0, was separated on a 1.5% agarose stacking gel buffered with 100 mM Tris-HCl at pH 7.0 and 1.9% agarose resolving gel buffered with 200 mM Tris-borate
25 at pH 8.3 under standard buffer conditions (anode buffer 1M Tris-HCl, pH 8.3; cathode buffer 0.025 M Tris, 0.192 M glycine). The gels were run at 13 mA constant current at 15°C until the phenol red tracking dye reached the end of the gel. Two protein bands were visualized in the agarose gels using Coomassie brilliant
30 blue staining.

The slower migrating band was referred to as "protein band 1" and faster migrating band was referred to as "protein band 2." The two protein bands were present in approximately equal amounts. The Coomassie stained agarose gels were used as a guide
35 to precisely excise the two protein bands from unstained portions of the gels. The excised pieces containing the protein bands were macerated and a small amount of sterile water was added. As a control, a portion of the gel that contained no protein was also excised and treated in the same manner as the gel pieces
40 containing the protein. Protein was recovered from the gel

pieces by electroelution into 100 mM Tris-borate pH 8.3, at 100 volts (constant voltage) for two hours. Alternatively, protein was passively eluted from the gel pieces by adding an equal volume of 50 mM Tris-HCl, pH 7.0, to the gel pieces, then
5 incubating at 30°C for 16 hours. This allowed the protein to diffuse from the gel into the buffer, which was then collected.

Results of insect toxicity tests using HPLC-purified toxin (33.6 min. peak) and agarose gel purified toxin demonstrated toxicity of the extracts. Injection of 1.5 µg of the HPLC
10 purified protein kills within 24 hours. Both protein bands 1 and 2, recovered from agarose gels by passive elution or electroelution, were lethal upon injection. The protein concentration estimated for these samples was less than 50 ng/larva. A comparison of the weight gain and the mortality
15 between the groups of larvae injected with protein bands 1 or 2 indicate that protein band 1 was more toxic by injection delivery.

When HPLC-purified toxin was applied to larval diet at a concentration of 7.5 µg/larva, it caused a halt in larval weight
20 gain (24 larvae tested). The larvae begin to feed, but after consuming only a very small portion of the toxin treated diet they began to show pathological symptoms induced by the toxin and the larvae cease feeding. The insect frass became discolored and most larva showed signs of diarrhea. Significant insect
25 mortality resulted when several 5 µg toxin doses were applied to the diet over a 7-10 day period.

Agarose-separated protein band 1 significantly inhibited larval weight gain at a dose of 200 ng/larva. Larvae fed similar concentrations of protein band 2 were not inhibited and gained
30 weight at the same rate as the control larvae. Twelve larvae were fed eluted protein and 45 larvae were fed protein-containing agarose pieces. These two sets of data indicate that protein band 1 was orally toxic to *Manduca sexta*. In this experiment it appeared that protein band 2 was not toxic to *Manduca sexta*.

35 Further analysis of protein bands 1 and 2 by SDS-PAGE under denaturing conditions showed that each band was composed of several smaller protein subunits. Proteins were visualized by Coomassie brilliant blue staining followed by silver staining to achieve maximum sensitivity.

The protein subunits in the two bands were very similar. Protein band 1 contains 8 protein subunits of 25.1, 56.2, 60.8, 65.6, 166, 171, 184 and 208 kDa. Protein band 2 had an identical profile except that the 25.1, 60.8, and 65.6 kDa proteins were not present. The 56.2, 60.8, 65.6, and 184 kDa proteins were present in the complex of protein band 1 at approximately equal concentrations and represent 80% or more of the total protein content of that complex.

The native HPLC-purified toxin was further characterized as follows. The toxin was heat labile in that after being heated to 60°C for 15 minutes it lost its ability to kill or to inhibit weight gain when injected or fed to *M. sexta* larvae. Assays were designed to detect lipase, type C phospholipase, nuclease or red blood cell hemolysis activities and were performed with purified toxin. None of these activities were present. Antibiotic zone inhibition assays were also done and the purified toxin failed to inhibit growth of Gram-negative or -positive bacteria, yeast or filamentous fungi, indicating that the toxic is not a xenorhabdin antibiotic.

The native HPLC-purified toxin was tested for ability to kill insects other than *Manduca sexta*. Table 2 lists insects killed by the HPLC-purified *P. luminescens* toxin in this study.

Table 2
Insects Killed by *P. luminescens* Toxin

	<u>Common Name</u>	<u>Order</u>	<u>Genus and species</u>	<u>Route of Delivery</u>
30	Tobacco horn worm	Lepidoptera	<i>Manduca sexta</i>	Oral and injected
	Mealworm	Coleoptera	<i>Tenebrio molitor</i>	Oral
35	Pharaoh ant	Hymenoptera	<i>Monomorium pharoanis</i>	Oral
	German cockroach	Dictyoptera	<i>Blattella germanica</i>	Oral and injected
40	Mosquito	Diptera	<i>Aedes aegypti</i>	Oral

Example 2
Insecticide Utility

The *Photorhabdus luminescens* utility and toxicity were
5 further characterized. *Photorhabdus luminescens* (strain W-14)
culture broth was produced as follows. The production medium was
2% Bacto Proteose Peptone[®] Number 3 (PP3, Difco Laboratories,
Detroit, Michigan) in Milli-Q[®] deionized water. Seed culture
10 flasks consisted of 175 ml medium placed in a 500 ml tribaffled
flask with a Delong neck, covered with a Kaput and autoclaved
for 20 minutes, T=250°F. Production flasks consisted of 500 mls
in a 2.8 liter 500 ml tribaffled flask with a Delong neck,
covered by a Shin-etsu silicon foam closure. These were
autoclaved for 45 minutes, T=250°F. The seed culture was
15 incubated at 28°C at 150 rpm in a gyrotory shaking incubator with
a 2 inch throw. After 16 hours of growth, 1% of the seed culture
was placed in the production flask which was allowed to grow for
24 hours before harvest. Production of the toxin appears to be
during log phase growth. The microbial broth was transferred to
20 a 1L centrifuge bottle and the cellular biomass was pelleted 130
minutes at 2500 RPM at 4°C, [R.C.F. = ~1600] HG-4L Rotor RC3
Sorval centrifuge, Dupont, Wilmington, Delaware). The primary
broth was chilled at 4°C for 8 - 16 hours and recentrifuged at
least 2 hours (conditions above) to further clarify the broth by
25 removal of a putative mucopolysaccharide which precipitated upon
standing. (An alternative processing method combined both steps
and involved the use of a 16 hour clarification centrifugation,
same conditions as above.) This broth was then stored at 4°C
prior to bioassay or filtration.
30 *Photorhabdus* culture broth and protein toxin(s) purified
from this broth showed activity (mortality and/or growth
inhibition, reduced adult emergence) against a number of insects.
More specifically, the activity is seen against corn rootworm
(larvae and adult), Colorado potato beetle, and turf grubs, which
35 are members of the insect order Coleoptera. Other members of the
Coleoptera include wireworms, pollen beetles, flea beetles, seed
beetles and weevils. Activity has also been observed against
aster leafhopper, which is a member of the order, Homoptera.
Other members of the Homoptera include planthoppers, pear psylla,
40 apple sucker, scale insects, whiteflies, and spittle bugs, as

- well as numerous host specific aphid species. The broth and purified fractions are also active against beet armyworm, cabbage looper, black cutworm, tobacco budworm, European corn borer, corn earworm, and codling moth, which are members of the order
- 5 *Lepidoptera*. Other typical members of this order are clothes moth, Indian mealmoth, leaf rollers, cabbage worm, cotton bollworm, bagworm, Eastern tent caterpillar, sod webworm, and fall armyworm. Activity is also seen against fruitfly and mosquito larvae, which are members of the order *Diptera*. Other
- 10 members of the order *Diptera* are pea midge, carrot fly, cabbage root fly, turnip root fly, onion fly, crane fly, house fly, and various mosquito species. Activity is seen against carpenter ant and Argentine ant, which are members of the order that also includes fire ants, odorous house ants, and little black ants.
- 15 The broth/fraction is useful for reducing populations of insects and were used in a method of inhibiting an insect population. The method may comprise applying to a locus of the insect an effective insect inactivating amount of the active described. Results are reported in Table 3.
- 20 Activity against corn rootworm larvae was tested as follows. *Photorhabdus* culture broth (filter sterilized, cell-free) or purified HPLC fractions were applied directly to the surface (~1.5 cm²) of 0.25 ml of artificial diet in 30 µl aliquots following dilution in control medium or 10 mM sodium phosphate
- 25 buffer, pH 7.0, respectively. The diet plates were allowed to air-dry in a sterile flow-hood and the wells were infested with single, neonate *Diabrotica undecimpunctata howardi* (Southern corn rootworm, SCR) hatched from sterilized eggs, with second instar SCR grown on artificial diet or with second instar *Diabrotica*
- 30 *virgifera virgifera* (Western corn rootworm, WCR) reared on corn seedlings grown in Metromix[®]. Second instar larvae were weighed prior to addition to the diet. The plates were sealed, placed in a humidified growth chamber and maintained at 27°C for the appropriate period (4 days for neonate and adult SCR, 2-5 days
- 35 for WCR larvae, 7-14 days for second instar SCR). Mortality and weight determinations were scored as indicated. Generally, 16 insects per treatment were used in all studies. Control mortalities were as follows: neonate larvae, <5%, adult beetles, 5%.

Activity against Colorado potato beetle was tested as follows. *Photorhabdus* culture broth or control medium was applied to the surface ($\sim 2.0 \text{ cm}^2$) of 1.5 ml of standard artificial diet held in the wells of a 24-well tissue culture plate. Each well received 50 μl of treatment and was allowed to air dry.

Individual second instar Colorado potato beetle (*Leptinotarsa decemlineata*, CPB) larvae were then placed onto the diet and mortality was scored after 4 days. Ten larvae per treatment were used in all studies. Control mortality was 3.3%.

Activity against Japanese beetle grubs and beetles was tested as follows. Turf grubs (*Popillia japonica*, 2-3rd instar) were collected from infested lawns and maintained in the laboratory in soil/peat mixture with carrot slices added as additional diet. Turf beetles were pheromone-trapped locally and maintained in the laboratory in plastic containers with maple leaves as food. Following application of undiluted *Photorhabdus* culture broth or control medium to corn rootworm artificial diet (30 $\mu\text{l}/1.54 \text{ cm}^2$, beetles) or carrot slices (larvae), both stages were placed singly in a diet well and observed for any mortality and feeding. In both cases there was a clear reduction in the amount of feeding (and feces production) observed.

Activity against mosquito larvae was tested as follows. The assay was conducted in a 96-well microtiter plate. Each well contained 200 μl of aqueous solution (*Photorhabdus* culture broth, control medium or H_2O) and approximately 20, 1-day old larvae (*Aedes aegypti*). There were 6 wells per treatment. The results were read at 2 hours after infestation and did not change over the three day observation period. No control mortality was seen.

Activity against fruitflies was tested as follows. Purchased *Drosophila melanogaster* medium was prepared using 50% dry medium and a 50% liquid of either water, control medium or *Photorhabdus* culture broth. This was accomplished by placing 8.0 ml of dry medium in each of 3 rearing vials per treatment and adding 8.0 ml of the appropriate liquid. Ten late instar *Drosophila melanogaster* maggots were then added to each vial. The vials were held on a laboratory bench, at room temperature, under fluorescent ceiling lights. Pupal or adult counts were made after 3, 7 and 10 days of exposure. Incorporation of *Photorhabdus* culture broth into the diet media for fruitfly

maggots caused a slight (17%) but significant reduction in day-10 adult emergence as compared to water and control medium (3% reduction).

Activity against aster leafhopper was tested as follows.

- 5 The ingestion assay for aster leafhopper (*Macrosteles severini*) is designed to allow ingestion of the active without other external contact. The reservoir for the active/"food" solution is made by making 2 holes in the center of the bottom portion of a 35 x 10 mm Petri dish. A 2 inch Parafilm M[®] square is placed
10 across the top of the dish and secured with an "O" ring. A 1 oz. plastic cup is then infested with approximately 7 leafhoppers and the reservoir is placed on top of the cup, Parafilm down. The test solution is then added to the reservoir through the holes. In tests using undiluted *Photorhabdus* culture broth, the broth
15 and control medium were dialyzed against water to reduce control mortality. Mortality is reported at day 2 where 26.5% control mortality was seen. In the tests using purified fractions (200 mg protein/ml) a final concentration of 5% sucrose was used in all treatments to improve survivability of the aster leafhoppers.
20 The assay was held in an incubator at 28°C, 70% RH with a 16/8 photoperiod. The assay was graded for mortality at 72 hours. Control mortality was 5.5%.

- Activity against Argentine ants was tested as follows. A 1.5 ml aliquot of 100% *Photorhabdus* culture broth, control medium
25 or water was pipetted into 2.0 ml clear glass vials. The vials were plugged with a piece of cotton dental wick that was moistened with the appropriate treatment. Each vial was placed into a separate 60x16mm Petri dish with 8 to 12 adult Argentine ants (*Linepithema humile*). There were three replicates per
30 treatment. Bioassay plates were held on a laboratory bench, at room temperature under fluorescent ceiling lights. Mortality readings were made after 5 days of exposure. Control mortality was 24%.

- Activity against carpenter ant was tested as follows. Black
35 carpenter ant workers (*Camponotus pennsylvanicus*) were collected from trees on DowElanco property in Indianapolis, IN. Tests with *Photorhabdus* culture broth were performed as follows. Each plastic bioassay container (7 1/8" x 3") held fifteen workers, a paper harborage and 10 ml of broth or control media in a plastic
40 shot glass. A cotton wick delivered the treatment to the ants

through a hole in the shot glass lid. All treatments contained 5% sucrose. Bioassays were held in the dark at room temperature and graded at 19 days. Control mortality was 9%. Assays delivering purified fractions utilized artificial ant diet mixed with the treatment (purified fraction or control solution) at a rate of 0.2 ml treatment/2.0 g diet in a plastic test tube. The final protein concentration of the purified fraction was less than 10 µg/g diet. Ten ants per treatment, a water source, harborage and the treated diet were placed in sealed plastic containers and maintained in the dark at 27°C in a humidified incubator. Mortality was scored at day 10. No control mortality was seen.

Activity against various lepidopteran larvae was tested as follows. *Photorhabdus* culture broth or purified fractions were applied directly to the surface (~1.5 cm²) of 0.25 ml of standard artificial diet in 30 µl aliquots following dilution in control medium or 10 mM sodium phosphate buffer, pH 7.0, respectively. The diet plates were allowed to air-dry in a sterile flow-hood and the wells were infested with single, neonate larva. European corn borer (*Ostrinia nubilalis*) and corn earworm (*Helicoverpa zea*) eggs were supplied from commercial sources and hatched in-house, whereas beet armyworm (*Spodoptera exigua*), cabbage looper (*Trichoplusia ni*), tobacco budworm (*Heliothis virescens*), codling moth (*Laspeyresia pomonella*) and black cutworm (*Agrotis ipsilon*) larvae were supplied internally. Following infestation with larvae, the diet plates were sealed, placed in a humidified growth chamber and maintained in the dark at 27°C for the appropriate period. Mortality and weight determinations were scored at days 5-7 for *Photorhabdus* culture broth and days 4-7 for the purified fraction. Generally, 16 insects per treatment were used in all studies. Control mortality ranged from 4-12.5% for control medium and was less than 10% for phosphate buffer.

Table 3

Effect of *Photorhabdus luminescens* (strain W-14)
Culture Broth and Purified Toxin Fraction on Mortality and Growth
Inhibition of Different Insect Orders/Species

5

Insect Order/Species	Broth		Purified Fraction	
	% Mort.	% G.I.	% Mort.	% G.I.
COLEOPTERA				
Corn Rootworm				
Southern/neonate larva	100	na	100	na
Southern/2 nd instar	na	38.5	nt	nt
Southern/adult	45	nt	nt	nt
Western/2 nd instar	na	35	nt	nt
Colorado Potato				
Beetle	93	nt	nt	nt
2 nd instar				
Turf Grub	na	a.f.	nt	nt
3 rd instar	na	a.f.	nt	nt
adult				
DIPTERA				
Fruit Fly (adult	17	nt	nt	nt
emergence)	100	na	nt	nt
Mosquito larvae				
HOMOPTERA				
Aster Leafhopper	96.5	na	100	na
HYMENOPTERA				
Argentine Ant	75	na	nt	na
Carpenter Ant	71	na	100	na
LEPIDOPTERA				
Beet Armyworm	12.5	36	18.75	41.4
Black Cutworm	nt	nt	0	71.2
Cabbage Looper	nt	nt	21.9	66.8
Codling Moth	nt	nt	6.25	45.9
Corn Earworm	56.3	94.2	97.9	na
European Corn Borer	96.7	98.4	100	na
Tobacco Budworm	13.5	52.5	19.4	85.6

Mort. = mortality, G.I. = growth inhibition,

na = not applicable, nt = not tested, a.f. = anti-feedant

Example 3Insecticide Utility Upon Soil Application

Photorhabdus luminescens (strain W-14) culture broth was
5 shown to be active against corn rootworm when applied directly to
soil or a soil-mix (Metromix®). Activity against neonate SCR and
WCR in Metromix® was tested as follows (Table 4). The test was
run using corn seedlings (United Agriseeds brand CL614) that were
germinated in the light on moist filter paper for 6 days. After
10 roots were approximately 3-6 cm long, a single kernel/seedling
was planted in a 591 ml clear plastic cup with 50 gm of dry
Metromix®. Twenty neonate SCR or WCR were then placed directly on
the roots of the seedling and covered with Metromix®. Upon
infestation, the seedlings were then drenched with 50 ml total
15 volume of a diluted broth solution. After drenching, the cups
were sealed and left at room temperature in the light for 7 days.
Afterwards, the seedlings were washed to remove all Metromix® and
the roots were excised and weighed. Activity was rated as the
percentage of corn root remaining relative to the control plants
20 and as leaf damage induced by feeding. Leaf damage was scored
visually and rated as either -, +, ++, or +++, with -
representing no damage and +++ representing severe damage.

Activity against neonate SCR in soil was tested as follows
(Table 5). The test was run using corn seedlings (United
25 Agriseeds brand CL614) that were germinated in the light on moist
filter paper for 6 days. After the roots were approximately 3-6
cm long, a single kernel/seedling was planted in a 591 ml clear
plastic cup with 150 gm of soil from a field in Lebanon, IN
planted the previous year with corn. This soil had not been
30 previously treated with insecticides. Twenty neonate SCR were
then placed directly on the roots of the seedling and covered
with soil. After infestation, the seedlings were drenched with
50 ml total volume of a diluted broth solution. After drenching,
the unsealed cups were incubated in a high relative humidity
35 chamber (80%) at 78°F. Afterwards, the seedlings were washed to
remove all soil and the roots were excised and weighed. Activity
was rated as the percentage of corn root remaining relative to
the control plants and as leaf damage induced by feeding. Leaf
damage was scored visually and rated as either -, +, ++, or +++,
40 with - representing no damage and +++ representing severe damage.

Table 4
Effect of *Photorhabdus luminescens* (strain W-14) Culture
Broth on Rootworm Larvae After Post-Infestation Drenching
(Metromix®)

5

	Treatment	Larvae	Leaf Damage	Root Weight (g)	%
	Southern Corn Rootworm				
10	Water	-	-	0.4916 ± 0.023	100
	Medium (2.0% v/v)	-	-	0.4416 ± 0.029	100
	Broth (6.25% v/v)	-	-	0.4641 ± 0.081	100
	Water	+	+++	0.1410 ± 0.006	28.7
15	Media (2.0% v/v)	+	+++	0.1345 ± 0.028	30.4
	Broth (1.56% v/v)	+	-	0.4830 ± 0.031	104
	Western Corn Rootworm				
20	Water	-	-	0.4446 ± 0.019	100
	Broth (2.0% v/v)	-	-	0.4069 ± 0.026	100
	Water	+	-	0.2202 ± 0.015	49
25	Broth (2.0% v/v)	+	-	0.3879 ± 0.013	95

Table 5
Effect of *Photorhabdus luminescens* (strain W-14) Culture Broth on
Southern Corn Rootworm Larvae After Post-Infestation Drenching
(Soil)

30

	Treatment	Larvae	Leaf Damage	Root Weight (g)	%
	Water	-	-	0.2148 ± 0.014	100
35	Broth (50% v/v)	-	-	0.2260 ± 0.016	103
	Water	+	+++	0.0916 ± 0.009	43
	Broth (50% v/v)	+	-	0.2428 ± 0.032	113

40 Activity of *Photorhabdus luminescens* (strain W-14) culture
broth against second instar turf grubs in Metromix® was observed
in tests conducted as follows (Table 6). Approximately 50 gm of
dry Metromix® was added to a 591 ml clear plastic cup. The
Metromix® was then drenched with 50 ml total volume of a 50% (v/v)
45 diluted *Photorhabdus* broth solution. The dilution of crude broth
was made with water, with 50% broth being prepared by adding 25
ml of crude broth to 25 ml of water for 50 ml total volume. A 1%
(w/v) solution of proteose peptone #3 (PP3), which is a 50%
dilution of the normal media concentration, was used as a broth
50 control. After drenching, five second instar turf grubs were

- placed on the top of the moistened Metromix[®]. Healthy turf grub larvae burrowed rapidly into the Metromix[®]. Those larvae that did not burrow within 1h were removed and replaced with fresh larvae. The cups were sealed and placed in a 28°C incubator, in the dark.
- 5 After seven days, larvae were removed from the Metromix[®] and scored for mortality. Activity was rated the percentage of mortality relative to control.

10 Table 6
Effect of *Photorhabdus luminescens* (strain W-14) Culture Broth on Turf Grub After Pre-Infestation Drenching (Metromix[®])

15	Treatment	Mortality*	Mortality %
	Water	7/15	47
	Control medium (1.0% w/v)	12/19	63
20	Broth (50% v/v)	17/20	85

25 *expressed as a ratio of dead/living larvae

Example 4
Insecticide Utility Upon Leaf Application

- 30 Activity of *Photorhabdus* broth against European corn borer was seen when the broth was applied directly to the surface of maize leaves (Table 7). In these assays *Photorhabdus* broth was diluted 100-fold with culture medium and applied manually to the surface of excised maize leaves at a rate of ~6.0 µl/cm² of leaf
- 35 surface. The leaves were air dried and cut into equal sized strips approximately 2 x 2 inches. The leaves were rolled, secured with paper clips and placed in 1 oz plastic shot glasses with 0.25 inch of 2% agar on the bottom surface to provide moisture. Twelve neonate European corn borers were then placed
- 40 onto the rolled leaf and the cup was sealed. After incubation for 5 days at 27°C in the dark, the samples were scored for feeding damage and recovered larvae.

Table 7

Effect of *Photorhabdus luminescens* (strain W-14) Culture Broth on European Corn Borer Larvae Following Pre-Infestation Application to Excised Maize Leaves

5

Treatment	Leaf Damage	Larvae Recovered	Weight(mg)
Water	Extensive	55/120	0.42 mg
Control Medium	Extensive	40/120	0.50 mg
Broth (1.0% v/v)	Trace	3/120	0.15 mg

10

Activity of the culture broth against neonate tobacco budworm (*Heliothis virescens*) was demonstrated using a leaf dip methodology. Fresh cotton leaves were excised from the plant and leaf disks were cut with an 18.5 mm cork-borer. The disks were individually emersed in control medium (PP3) or *Photorhabdus luminescens* (strain W-14) culture broth which had been concentrated approximately 10-fold using an Amicon (Beverly, MA), Proflux M12 tangential filtration system with a 10 kDa filter. Excess liquid was removed and a straightened paper clip was placed through the center of the disk. The paper clip was then wedged into a plastic, 1.0 oz shot glass containing approximately 2.0 ml of 1% Agar. This served to suspend the leaf disk above the agar. Following drying of the leaf disk, a single neonate tobacco budworm larva was placed on the disk and the cup was capped. The cups were then sealed in a plastic bag and placed in a darkened, 27°C incubator for 5 days. At this time the remaining larvae and leaf material were weighed to establish a measure of leaf damage (Table 8).

30

Table 8

Effect of *Photorhabdus luminescens* (Strain W-14) Culture Broth on Tobacco Budworm Neonates in a Cotton-Leaf Dip Assay

Treatment	Leaf Disk	Final Weights (mg)
		Larvae
Control leaves	55.7 ± 1.3	na*
Control Medium	34.0 ± 2.9	4.3 ± 0.91
<i>Photorhabdus</i> broth	54.3 ± 1.4	0.0**

* - not applicable, ** - no live larvae found

40

Example 5. Part A
Characterization of Toxin Peptide Components

In a subsequent analysis, the toxin protein subunits of the
5 bands isolated as in Example 1 were resolved on a 7% SDS
polyacrylamide electrophoresis gel with a ratio of 30:0.8
(acrylamide:BIS-acrylamide). This gel matrix facilitates better
resolution of the larger proteins. The gel system used to
estimate the Band 1 and Band 2 subunit molecular weights in
10 Example 1 was an 18% gel with a ratio of 38:0.18 (acrylamide:BIS-
acrylamide), which allowed for a broader range of size
separation, but less resolution of higher molecular weight
components.

In this analysis, 10, rather than 8, protein bands were
15 resolved. Table 9 reports the calculated molecular weights of
the 10 resolved bands, and directly compares the molecular
weights estimated under these conditions to those of the prior
example. It is not surprising that additional bands were
detected under the different separation conditions used in this
20 example. Variations between the prior and new estimates of
molecular weight are also to be expected given the differences in
analytical conditions. In the analysis of this example, it is
thought that the higher molecular weight estimates are more
accurate than in Example 1, as a result of improved resolution.
25 However, these are estimates based on SDS PAGE analysis, which
are typically not analytically precise and result in estimates of
peptides and which may have been further altered due to post- and
co-translational modifications.

Amino acid sequences were determined for the N-terminal
30 portions of five of the 10 resolved peptides. Table 9 correlates
the molecular weight of the proteins and the identified
sequences. In SEQ ID NO:2, certain analyses suggest that the
proline at residue 5 may be an asparagine (asn). In SEQ ID NO:3,
certain analyses suggest that the amino acid residues at
35 positions 13 and 14 are both arginine (arg). In SEQ ID NO:4,
certain analyses suggest that the amino acid residue at position
6 may be either alanine (ala) or serine (ser). In SEQ ID NO:5,
certain analyses suggest that the amino acid residue at position
3 may be aspartic acid (asp).

40

Table 9

EXAMPLE 1		
<u>ESTIMATE</u>	<u>NEW ESTIMATE*</u>	<u>SEQ. LISTING</u>
208	200.2 kDa	SEQ ID NO:1
184	175.0 kDa	SEQ ID NO:2
65.6	68.1 kDa	SEQ ID NO:3
60.8	65.1 kDa	SEQ ID NO:4
56.2	58.3 kDa	SEQ ID NO:5
25.1	23.2 kDa	SEQ ID NO:15
*New estimates are based on SDS PAGE and are not based on gene sequences. SDS PAGE is not analytically precise.		

Example 5, Part BCharacterization of Toxin Peptide Components

15

New N-terminal sequence, SEQ ID NO:15, Ala Gln Asp Gly Asn Gln Asp Thr Phe Phe Ser Gly Asn Thr, was obtained by further N-terminal sequencing of peptides isolated from Native HPLC-purified toxin as described in Example 5, Part A, above. This peptide comes from the *tcaA* gene. The peptide labeled TcaA_{ii}, starts at position 254 and goes to position 491, where the TcaA_{iii} peptide starts, SEQ ID NO:4. The estimated size of the peptide based on the gene sequence is 25,240 Da.

25

Example 6Characterization of Toxin Peptide Components

In yet another analysis, the toxin protein complex was re-isolated from the *Photorhabdus luminescens* growth medium (after culture without Tween) by performing a 10% - 80% ammonium sulfate precipitation followed by an ion exchange chromatography step (Mono Q) and two molecular sizing chromatography steps. These conditions were like those used in Example 1. During the first molecular sizing step, a second biologically active peak was found at about 100 ± 10 kDa. Based upon protein measurements, this fraction was 20 - 50 fold less active than the larger, or primary, active peak of about 860 ± 100 kDa (native). During this isolation experiment, a smaller active peak of about 325 ± 50 kDa that retained a considerable portion of the starting biological activity was also resolved. It is thought that the 325 kDa peak is related to or derived from the 860 kDa peak.

A 56 kDa protein was resolved in this analysis. The N-terminal sequence of this protein is presented in SEQ ID NO:6. It is noteworthy that this protein shares significant identity and conservation with SEQ ID NO:5 at the N-terminus, suggesting that the two may be encoded by separate members of a gene family and that the proteins produced by each gene are sufficiently similar to both be operable in the insecticidal toxin complex.

A second, prominent 185 kDa protein was consistently present in amounts comparable to that of protein 3 from Table 9, and may be the same protein or protein fragment. The N-terminal sequence of this 185 kDa protein is shown at SEQ ID NO:7.

Additional N-terminal amino acid sequence data were also obtained from isolated proteins. None of the determined N-terminal sequences appear identical to a protein identified in Table 9. Other proteins were present in isolated preparation. One such protein has an estimated molecular weight of 108 kDa and an N-terminal sequence as shown in SEQ ID NO:8. A second such protein has an estimated molecular weight of 80 kDa and an N-terminal sequence as shown in SEQ ID NO:9.

When the protein material in the approximately 325 kDa active peak was analyzed by size, bands of approximately 51, 31, 28, and 22 kDa were observed. As in all cases in which a molecular weight was determined by analysis of electrophoretic mobility, these molecular weights were subject to error effects introduced by buffer ionic strength differences, electrophoresis power differences, and the like. One of ordinary skill would understand that definitive molecular weight values cannot be determined using these standard methods and that each was subject to variation. It was hypothesized that proteins of these sizes are degradation products of the larger protein species (of approximately 200 kDa size) that were observed in the larger primary toxin complex.

Finally, several preparations included a protein having the N-terminal sequence shown in SEQ ID NO:10. This sequence was strongly homologous to known chaperonin proteins, accessory proteins known to function in the assembly of large protein complexes. Although the applicants could not ascribe such an assembly function to the protein identified in SEQ ID NO:10, it was consistent with the existence of the described toxin protein complex that such a chaperonin protein could be involved in its

assembly. Moreover, although such proteins have not directly been suggested to have toxic activity, this protein may be important to determining the overall structural nature of the protein toxin, and thus, may contribute to the toxic activity or durability of the complex in vivo after oral delivery.

Subsequent analysis of the stability of the protein toxin complex to proteinase K was undertaken. It was determined that after 24 hour incubation of the complex in the presence of a 10-fold molar excess of proteinase K, activity was virtually eliminated (mortality on oral application dropped to about 5%). These data confirm the proteinaceous nature of the toxin.

The toxic activity was also retained by a dialysis membrane, again confirming the large size of the native toxin complex.

15

Example 7

Isolation, Characterization and Partial Amino Acid Sequencing of *Photorhabdus* Toxins

Isolation and N-Terminal Amino Acid Sequencing: In a set of experiments conducted in parallel to Examples 5 and 6, ammonium sulfate precipitation of *Photorhabdus* proteins was performed by adjusting *Photorhabdus* broth, typically 2-3 liters, to a final concentration of either 10% or 20% by the slow addition of ammonium sulfate crystals. After stirring for 1 hour at 4°C, the material was centrifuged at 12,000 x g for 30 minutes. The supernatant was adjusted to 80% ammonium sulfate, stirred at 4°C for 1 hour, and centrifuged at 12,000 x g for 60 minutes. The pellet was resuspended in one-tenth the volume of 10 mM Na₂·PO₄, pH 7.0 and dialyzed against the same phosphate buffer overnight at 4°C. The dialyzed material was centrifuged at 12,000 x g for 1 hour prior to ion exchange chromatography.

A HR 16/50 Q Sepharose (Pharmacia) anion exchange column was equilibrated with 10 mM Na₂·PO₄, pH 7.0. Centrifuged, dialyzed ammonium sulfate pellet was applied to the Q Sepharose column at a rate of 1.5 ml/min and washed extensively at 3.0 ml/min with equilibration buffer until the optical density (O.D. 280) reached less than 0.100. Next, either a 60 minute NaCl gradient ranging from 0 to 0.5 M at 3 ml/min, or a series of step elutions using 0.1 M, 0.4 M and finally 1.0 NaCl for 60 minutes each was applied to the column. Fractions were pooled and concentrated using a

Centriprep 100. Alternatively, proteins could be eluted by a single 0.4 M NaCl wash without prior elution with 0.1 M NaCl.

Two milliliter aliquots of concentrated Q Sepharose samples were loaded at 0.5 ml/min onto a HR 16/50 Superose 12 (Pharmacia) gel filtration column equilibrated with 10 mM Na_2PO_4 , pH 7.0. The column was washed with the same buffer for 240 min at 0.5 ml/min and 2 min samples were collected. The void volume material was collected and concentrated using a Centriprep 100. Two milliliter aliquots of concentrated Superose 12 samples were loaded at 0.5 ml/min onto a HR 16/50 Sepharose 4B-CL (Pharmacia) gel filtration column equilibrated with 10 mM Na_2PO_4 , pH 7.0. The column was washed with the same buffer for 240 min at 0.5 ml/min and 2 min samples were collected.

The excluded protein peak was subjected to a second fractionation by application to a gel filtration column that used a Sepharose CL-4B resin, which separates proteins ranging from ~30 kDa to 1000 kDa. This fraction was resolved into two peaks; a minor peak at the void volume (>1000 kDa) and a major peak which eluted at an apparent molecular weight of about 860 kDa. Over a one week period subsequent samples subjected to gel filtration showed the gradual appearance of a third peak (approximately 325 kDa) that seemed to arise from the major peak, perhaps by limited proteolysis. Bioassays performed on the three peaks showed that the void peak had no activity, while the 860 kDa toxin complex fraction was highly active, and the 325 kDa peak was less active, although quite potent. SDS PAGE analysis of Sepharose CL-4B toxin complex peaks from different fermentation productions revealed two distinct peptide patterns, denoted "P" and "S". The two patterns had marked differences in the molecular weights and concentrations of peptide components in their fractions. The "S" pattern, produced most frequently, had 4 high molecular weight peptides (> 150 kDa) while the "P" pattern had 3 high molecular weight peptides. In addition, the "S" peptide fraction was found to have 2-3 fold more activity against European Corn Borer. This shift may be related to variations in protein expression due to age of inoculum and/or other factors based on growth parameters of aged cultures.

Milligram quantities of peak toxin complex fractions determined to be "P" or "S" peptide patterns were subjected to preparative SDS PAGE, and transblotted with TRIS-glycine

(Seprabuff™ to PVDF membranes (ProBlott™, Applied Biosystems) for 3-4 hours. Blots were sent for amino acid analysis and N-terminal amino acid sequencing at Harvard MicroChem and Cambridge ProChem, respectively. Three peptides in the "S" pattern had
5 unique N-terminal amino acid sequences compared to the sequences identified in the previous example. A 201 kDa (TcdAii) peptide set forth as SEQ ID NO:13 below shared between 33% amino acid identity and 50% similarity with SEQ ID NO:1 (TcbAii) (Table 10, in Table 10 vertical lines denote amino acid identities and
10 colons indicate conservative amino acid substitutions). A second peptide of 197 kDa, SEQ ID NO:14 (TcdB), had 42% identity and 58% homology with SEQ ID NO:2 (TcaC). Yet a third peptide of 205 kDa was denoted TcdAii. In addition, a limited N-terminal amino acid sequence, SEQ ID NO:16 (TcbA), of a peptide of at least 235 kDa
15 was identical in homology with the amino acid sequence, SEQ ID NO:12, deduced from a cloned gene (tcbA), SEQ ID NO:11, containing a deduced amino acid sequence corresponding to SEQ ID NO:1 (TcbAii). This indicates that the larger 235+ kDa peptide was proteolytically processed to the 201 kDa peptide, (TcbAii),
20 (SEQ ID NO:1) during fermentation, possibly resulting in activation of the molecule. In yet another sequence, the sequence originally reported as SEQ ID NO:5 (TcaBii) reported in Example 5 above, was found to contain an aspartic acid residue (Asp) at the third position rather than glycine (Gly) and two
25 additional amino acids Gly and Asp at the eighth and ninth positions, respectively. In yet two other sequences, SEQ ID NO:2 (TcaC) and SEQ ID NO:3 (TcaB_i), additional amino acid sequence was obtained. Densitometric quantitation was performed using a sample that was identical to the "S" preparation sent for N-
30 terminal analysis. This analysis showed that the 201 kDa and 197 kDa peptides represent 7.0% and 7.2%, respectively, of the total Coomassie brilliant blue stained protein in the "S" pattern and are present in amounts similar to the other abundant peptides. It is speculated that these peptides may represent protein
35 homologs, analogous to the situation found with other bacterial toxins, such as various CryI Bt toxins. These proteins vary from 40-90% homology at their N-terminal amino acid sequence, which encompasses the toxic fragment.

Internal Amino Acid Sequencing: To facilitate cloning of toxin peptide genes, internal amino acid sequences of selected peptides were obtained as followed. Milligram quantities of peak 2A fractions determined to be "P" or "S" peptide patterns were subjected to preparative SDS PAGE, and transblotted with TRIS-glycine (Seprabuff™ to PVDF membranes (ProBlott™, Applied Biosystems) for 3-4 hours. Blots were sent for amino acid analysis and N-terminal amino acid sequencing at Harvard MicroChem and Cambridge ProChem, respectively. Three peptides, referred to as TcbA_{ii} (containing SEQ ID NO:1), TcdA_{ii}, and TcaB_i (containing SEQ ID NO:3) were subjected to trypsin digestion by Harvard MicroChem followed by HPLC chromatography to separate individual peptides. N-terminal amino acid analysis was performed on selected tryptic peptide fragments. Two internal peptides were sequenced for the peptide TcaB_i (205 kDa peptide) referred to as TcaB_i-PT111 (SEQ ID NO:17) and TcaB_i-PT79 (SEQ ID NO:18). Two internal peptides were sequenced for the peptide TcaB_i (68 kDa peptide) referred to as TcaB_i-PT158 (SEQ ID NO:19) and TcaB_i-PT108 (SEQ ID NO:20). Four internal peptides were sequenced for the peptide TcbA_{ii} (201 kDa peptide) referred to as TCBAII-PT103 (SEQ ID NO:21), TcbA_{ii}-PT56 (SEQ ID NO:22), TcbA_{ii}-PT81(a) (SEQ ID NO:23), and TcbA_{ii}-PT81(b) (SEQ ID NO:24).

Table 10
N-Terminal Amino Acid Sequences

201 kDa (33% identity & 50% similarity to SEQ ID NO.1)	
L I G Y N N Q F S G * A	SEQ ID NO:13
:	:
F I Q G Y S D L F G N - A	SEQ ID NO:1
197 kDa (42% identity & 58% similarity SEQ ID NO.2)	
M Q N S Q T F S V G E L	SEQ ID NO.14
:	:
M Q D S P E V S I T T L	SEQ ID NO.2

Example 8

Construction of a cosmid library of *Photobacterium luminescens* W-14 genomic DNA and its screening to isolate genes encoding peptides comprising the toxic protein preparation

As a prerequisite for the production of *Photobacterium* insect toxic proteins in heterologous hosts, and for other uses, it is necessary to isolate and characterize the genes that encode those

peptides. This objective was pursued in parallel. One approach, described later, was based on the use of monoclonal and polyclonal antibodies raised against the purified toxin which were then used to isolate clones from an expression library. The other approach, described in this example, is based on the use of the N-terminal and internal amino acid sequence data to design degenerate oligonucleotides for use in PCR amplification. Either method can be used to identify DNA clones that contain the peptide-encoding genes so as to permit the isolation of the respective genes, and the determination of their DNA base sequence.

GENOMIC DNA ISOLATION: *Photorhabdus luminescens* strain W-14 (ATCC accession number 55397) was grown on 2% proteose peptone #3 agar (Difco Laboratories, Detroit, MI) and insecticidal toxin competence was maintained by repeated bioassay after passage, using the method described in Example 1 above. A 50 ml shake culture was produced in a 175 ml baffled flask in 2% proteose peptone #3 medium, grown at 28°C and 150 rpm for approximately 24 hours. 15 ml of this culture was pelleted and frozen in its medium at -20°C until it was thawed for DNA isolation. The thawed culture was centrifuged, (700 x g, 30 min) and the floating orange mucopolysaccharide material was removed. The remaining cell material was centrifuged (25,000 x g, 15 min) to pellet the bacterial cells, and the medium was removed and discarded.

Genomic DNA was isolated by an adaptation of the CTAB method described in section 2.4.1 of Current Protocols in Molecular Biology (Ausubel et al. eds, John Wiley & Sons, 1994) [modified to include a salt shock and with all volumes increased 10-fold]. The pelleted bacterial cells were resuspended in TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0) to a final volume of 10 ml, then 12 ml of 5 M NaCl was added; this mixture was centrifuged 20 min at 15,000 x g. The pellet was resuspended in 5.7 ml TE and 300 ml of 10% SDS and 60 ml of 20 mg/ml proteinase K (Gibco BRL Products, Grand Island, NY; in sterile distilled water) were added to the suspension. This mixture was incubated at 37°C for 1 hr; then approximately 10 mg lysozyme (Worthington Biochemical Corp., Freehold, NJ) was added. After an additional 45 min, 1 ml of 5 M NaCl and 800 ml of CTAB/NaCl solution (10% w/v CTAB, 0.7 M

NaCl) were added. This preparation was incubated 10 min at 65°C, then gently agitated and further incubated and agitated for approximately 20 min to assist clearing of the cellular material. An equal volume of chloroform/isoamyl alcohol solution (24:1, v/v) was added, mixed gently and centrifuged. After two extractions with an equal volume of PCI (phenol/chloroform/isoamyl alcohol; 50:49:1, v/v/v; equilibrated with 1 M Tris-HCl, pH 8.0; Intermountain Scientific Corporation, Kaysville, UT), the DNA was precipitated with 0.6 volume of isopropanol. The DNA precipitate was gently removed with a glass rod, washed twice with 70% ethanol, dried, and dissolved in 2 ml STE (10 mM Tris-HCl pH 8.0, 10 mM NaCl, 1 mM EDTA). This preparation contained 2.5 mg/ml DNA, as determined by optical density at 260 nm (i.e., OD₂₆₀).

The molecular size range of the isolated genomic DNA was evaluated for suitability for library construction. CHEF gel analysis was performed in 1.5% agarose (Seakem® LE, FMC BioProducts, Rockland, ME) gels with 0.5 X TBE buffer (44.5 mM Tris-HCl pH 8.0, 44.5 mM H₃BO₃, 1 mM EDTA) on a BioRad CHEF-DR II apparatus with a Pulsewave 760 Switcher (Bio-Rad Laboratories, Inc., Richmond, CA). The running parameters were: initial A time, 3 sec; final A time, 12 sec; 200 volts; running temperature, 4-18°C; run time, 16.5 hr. Ethidium bromide staining and examination of the gel under ultraviolet light indicated the DNA ranged from 30-250 kbp in size.

CONSTRUCTION OF LIBRARY: A partial Sau3A 1 digest was made of this *Photorhabdus* genomic DNA preparation. The method was based on section 3.1.3 of Ausubel (supra.). Adaptions included running smaller scale reactions under various conditions until nearly optimal results were achieved. Several scaled-up large reactions with varied conditions were run, the results analyzed on CHEF gels, and only the best large scale preparation was carried forward. In the optimal case, 200 µg of *Photorhabdus* genomic DNA was incubated with 1.5 units of Sau3A 1 (New England Biolabs, "NEB", Beverly, MA) for 15 min at 37°C in 2 ml total volume of 1X NEB 4 buffer (supplied as 10X by the manufacturer). The reaction was stopped by adding 2 ml of PCI and centrifuging at 8000 x g for 10 min. To the supernatant were added 200 µl of 5 M NaCl plus 6 ml of ice-cold ethanol. This preparation was

chilled for 30 min at -20°C , then centrifuged at $12,000 \times g$ for 15 min. The supernatant was removed and the precipitate was dried in a vacuum oven at 40°C , then resuspended in 400 μl STE. Spectrophotometric assay indicated about 40% recovery of the input DNA. The digested DNA was size fractionated on a sucrose gradient according to section 5.3.2 of CPMB (op. cit.). A 10% to 40% (w/v) linear sucrose gradient was prepared with a gradient maker in Ultra-Clear™ tubes (Beckman Instruments, Inc., Palo Alto, CA) and the DNA sample was layered on top. After centrifugation, (26,000 rpm, 17 hr, Beckman SW41 rotor, 20°C), fractions (about 750 μl) were drawn from the top of the gradient and analyzed by CHEF gel electrophoresis (as described earlier). Fractions containing Sau3A 1 fragments in the size range 20-40 kbp were selected and DNA was precipitated by a modification (amounts of all solutions increased approximately 6.3-fold) of the method in section 5.3.3 of Ausubel (supra.). After overnight precipitation, the DNA was collected by centrifugation ($17,000 \times g$, 15 min), dried, redissolved in TE, pooled into a final volume of 80 μl , and reprecipitated with the addition of 8 μl 3 M sodium acetate and 220 μl ethanol. The pellet collected by centrifugation as above was resuspended in 12 μl TE. Concentration of the DNA was determined by Hoechst 33258 dye (Polysciences, Inc., Warrington, PA) fluorometry in a Hoefer TKO100 fluorimeter (Hoefer Scientific Instruments, San Francisco, CA). Approximately 2.5 μg of the size-fractionated DNA was recovered.

Thirty μg of cosmid pWE15 DNA (Stratagene, La Jolla, CA) was digested to completion with 100 units of restriction enzyme BamH 1 (NEB) in the manufacturer's buffer (final volume of 200 μl , 37°C , 1 hr). The reaction was extracted with 100 μl of PCI and DNA was precipitated from the aqueous phase by addition of 20 μl 3M sodium acetate and 550 μl -20°C absolute ethanol. After 20 min at -70°C , the DNA was collected by centrifugation ($17,000 \times g$, 15 min), dried under vacuum, and dissolved in 180 μl of 10 mM Tris-HCl, pH 8.0. To this were added 20 μl of 10X CIP buffer (100 mM Tris-HCl, pH 8.3; 10 mM ZnCl_2 ; 10 mM MgCl_2), and 1 μl (0.25 units) of 1:4 diluted calf intestinal alkaline phosphatase

(Boehringer Mannheim Corporation, Indianapolis, IN). After 30 min at 37°C, the following additions were made: 2 µl 0.5 M EDTA, pH 8.0; 10 µl 10% SDS; 0.5 µl of 20 mg/ml proteinase K (as above), followed by incubation at 55°C for 30 min. Following sequential extractions with 100 µl of PCI and 100 µl phenol (Intermountain Scientific Corporation, equilibrated with 1 M Tris-HCl, pH 8.0), the dephosphorylated DNA was precipitated by addition of 72 µl of 7.5 M ammonium acetate and 550 µl -20°C ethanol, incubation on ice for 30 min, and centrifugation as above. The pelleted DNA was washed once with 500 µl -20°C 70% ethanol, dried under vacuum, and dissolved in 20 µl of TE buffer.

Ligation of the size-fractionated Sau3A 1 fragments to the BamH 1-digested and phosphatased pWE15 vector was accomplished using T4 ligase (NEB) by a modification (i.e., use of premixed 10X ligation buffer supplied by the manufacturer) of the protocol in section 3.33 of Ausubel. Ligation was carried out overnight in a total volume of 20 µl at 15°C, followed by storage at -20°C.

Four µl of the cosmid DNA ligation reaction, containing about 1 µg of DNA, was packaged into bacteriophage lambda using a commercial packaging extract (Gigapack[®] III Gold Packaging Extract, Stratagene), following the manufacturer's directions. The packaged preparation was stored at 4°C until use. The packaged cosmid preparation was used to infect *Escherichia coli* XL1 Blue MR cells (Stratagene) according to the Gigapack[®] III Gold protocols ("Titering the Cosmid Library"), as follows. XL1 Blue MR cells were grown in LB medium (g/L: Bacto-tryptone, 10; Bacto-yeast extract, 5; Bacto-agar, 15; NaCl, 5; [Difco Laboratories, Detroit, MI]) containing 0.2% (w/v) maltose plus 10 mM MgSO₄, at 37°C. After 5 hr growth, cells were pelleted at 700 x g (15 min) and resuspended in 6 ml of 10 mM MgSO₄. The culture density was adjusted with 10 mM MgSO₄ to OD₆₀₀ = 0.5. The packaged cosmid library was diluted 1:10 or 1:20 with sterile SM medium (0.1 M NaCl, 10 mM MgSO₄, 50 mM Tris-HCl pH 7.5, 0.01% w/v gelatin), and 25 µl of the diluted preparation was mixed with 25 µl of the diluted XL1 Blue MR cells. The mixture was incubated at 25°C for 30 min (without shaking), then 200 µl of LB broth was added, and incubation was continued for approximately 1 hr with occasional

gentle shaking. Aliquots (20-40 μ l) of this culture were spread on LB agar plates containing 100 mg/l ampicillin (i.e., LB-Amp₁₀₀) and incubated overnight at 37°C. To store the library without amplification, single colonies were picked and inoculated into individual wells of sterile 96-well microwell plates; each well containing 75 μ l of Terrific Broth (TB media: 12 g/l Bacto-tryptone, 24 g/l Bacto-yeast extract, 0.4% v/v glycerol, 17 mM KH₂PO₄, 72 mM K₂HPO₄) plus 100 mg/l ampicillin (i.e., TB-Amp₁₀₀) and incubated (without shaking) overnight at 37°C. After replicating the 96-well plate into a copy plate, 75 μ l/well of filter-sterilized TB:glycerol (1:1, v/v; with, or without, 100 mg/l ampicillin) was added to the plate, it was shaken briefly at 100 rpm, 37°C, and then closed with Parafilm® (American National Can, Greenwich, CT) and placed in a -70°C freezer for storage. Copy plates were grown and processed identically to the master plates. A total of 40 such master plates (and their copies) were prepared.

SCREENING OF THE LIBRARY WITH RADIOLABELED DNA PROBES: To prepare colony filters for probing with radioactively labeled probes, ten 96-well plates of the library were thawed at 25°C (bench top at room temperature). A replica plating tool with 96 prongs was used to inoculate a fresh 96-well copy plate containing 75 μ l/well of TB-Amp₁₀₀. The copy plate was grown overnight (stationary) at 37°C, then shaken about 30 min at 100 rpm at 37°C. A total of 800 colonies was represented in these copy plates, due to nongrowth of some isolates. The replica tool was used to inoculate duplicate impressions of the 96-well arrays onto Magna NT (MSI, Westboro, MA) nylon membranes (0.45 micron, 220 x 250 mm) which had been placed on solid LB-Amp₁₀₀ (100 ml/dish) in Bio-assay plastic dishes (Nunc, 243 x 243 x 18 mm; Curtin Mathison Scientific, Inc., Wood Dale, IL). The colonies were grown on the membranes at 37°C for about 3 hr.

A positive control colony (a bacterial clone containing a GZ4 sequence insert, see below) was grown on a separate Magna NT membrane (Nunc, 0.45 micron, 82 mm circle) on LB medium supplemented with 35 mg/l chloramphenicol (i.e., LB-Cam₃₅), and processed alongside the library colony membranes. Bacterial colonies on the membranes were lysed, and the DNA was denatured

and neutralized according to a protocol taken from the Genius™ System User's Guide version 2.0 (Boehringer Mannheim, Indianapolis, IN). Membranes were placed colony side up on filter paper soaked with 0.5 N NaOH plus 1.5 M NaCl for 15 min to denature, and neutralized on filter paper soaked with 1 M Tris-HCl pH 8.0, 1.5 M NaCl for 15 min. After UV-crosslinking using a Stratagene UV Stratalinker set on auto crosslink, the membranes were stored dry at 25°C until use. Membranes were trimmed into strips containing the duplicate impressions of a single 96-well plate, then washed extensively by the method of section 6.4.1 in CPMB (*op. cit.*): 3 hr at 25°C in 3X SSC, 0.1% (w/v) SDS, followed by 1 hr at 65°C in the same solution, then rinsed in 2X SSC in preparation for the hybridization step (20X SSC = 3 M NaCl, 0.3 M sodium citrate, pH 7.0).

15

Amplification of a specific genomic fragment of a *tcaC* gene.

Based on the N-terminal amino acid sequence determined for the purified TcaC peptide fraction [disclosed herein as SEQ ID NO:2], a pool of degenerate oligonucleotides (pool S4Psh) was synthesized by standard β -cyanoethyl chemistry on an Applied BioSystem ABI394 DNA/RNA Synthesizer (Perkin Elmer, Foster City, CA). The oligonucleotides were deprotected 8 hours at 55°C, dissolved in water, quantitated by spectrophotometric measurement, and diluted for use. This pool corresponds to the determined N-terminal amino acid sequence of the TcaC peptide. The determined amino acid sequence and the corresponding degenerate DNA sequence are given below, where A, C, G, and T are the standard DNA bases, and I represents inosine:

30	Amino Acid	Met	Gln	Asp	Ser	Pro	Glu	Val
	S4Psh	5' ATG	CA(A/G)	GA(T/C)	(T/A)(C/G)(T/A)	CCI	GA(A/G)	GT 3'

Another set of degenerate oligonucleotides was synthesized (pool P2.3.5R), representing the complement of the coding strand for the determined amino acid sequence of the SEQ ID NO:17:

40	Amino Acid	Ala	Phe	Asn	Ile	Asp	Asp	Val
	Codons	5' GCN	TT(T/C)	AA(T/C)	AT(A/T/C)	GA(T/C)	GA(T/C)	GT 3'
	P2.3.5R	3' CG(A/C/G/T)	AA(A/G)	TT(A/G)	TA(T/A/G)	CT(A/G)	CT(A/G)	CA 5'

These oligonucleotides were used as primers in Polymerase Chain Reactions (PCR®, Roche Molecular Systems, Branchburg, NJ) to

amplify a specific DNA fragment from genomic DNA prepared from *Photorhabdus* strain W-14 (see above). A typical reaction (50 μ l) contained 125 pmol of each primer pool P2Psh and P2.3.5R, 253 ng of genomic template DNA, 10 nmol each of dATP, dCTP, dGTP, and dTTP, 1X GeneAmp[®] PCR buffer, and 2.5 units of AmpliTaq[®] DNA polymerase (both from Roche Molecular Systems; 10X GeneAmp[®] buffer is 100 mM Tris-HCl pH 8.3, 500 mM KCl, 0.01% w/v gelatin). Amplifications were performed in a Perkin Elmer Cetus DNA Thermal Cycler (Perkin Elmer, Foster City, CA) using 35 cycles of 94°C (1.0 min), 55°C (2.0 min), 72°C (3.0 min), followed by an extension period of 7.0 min at 72°C. Amplification products were analyzed by electrophoresis through 2% w/v NuSieve[®] 3:1 agarose (FMC BioProducts) in TEA buffer (40 mM Tris-acetate, 2 mM EDTA, pH 8.0). A specific product of estimated size 250 bp was observed amongst numerous other amplification products by ethidium bromide (0.5 μ g/ml) staining of the gel and examination under ultraviolet light.

The region of the gel containing an approximately 250 bp product was excised, and a small plug (0.5 mm dia.) was removed and used to supply template for PCR amplification (40 cycles). The reaction (50 μ l) contained the same components as above, minus genomic template DNA. Following amplification, the ends of the fragments were made blunt and were phosphorylated by incubation at 25°C for 20 min with 1 unit of T4 DNA polymerase (NEB), 1 nmol ATP, and 2.15 units of T4 kinase (Pharmacia Biotech Inc., Piscataway, NJ).

DNA fragments were separated from residual primers by electrophoresis through 1% w/v GTG[®] agarose (FMC) in TEA. A gel slice containing fragments of apparent size 250 bp was excised, and the DNA was extracted using a Qiaex kit (Qiagen Inc., Chatsworth, CA).

The extracted DNA fragments were ligated to plasmid vector pBC KS(+) (Stratagene) that had been digested to completion with restriction enzyme Sma I and extracted in a manner similar to that described for pWE15 DNA above. A typical ligation reaction (16.3 μ l) contained 100 ng of digested pBC KS(+) DNA, 70 ng of 250 bp fragment DNA, 1 nmol [Co(NH₃)₆]Cl₂, and 3.9 Weiss units of T4 DNA ligase (Collaborative Biomedical Products, Bedford, MA), in 1X ligation buffer (50 mM Tris-HCl, pH 7.4; 10 mM MgCl₂; 10 mM

dithiothreitol; 1 mM spermidine, 1 mM ATP, 100 mg/ml bovine serum albumin). Following overnight incubation at 14°C, the ligated products were transformed into frozen, competent *Escherichia coli* DH5α cells (Gibco BRL) according to the suppliers' recommendations, and plated on LB-Camp plates, containing IPTG (119 µg/ml) and X-gal (50 µg/ml). Independent white colonies were picked, and plasmid DNA was prepared by a modified alkaline-lysis/PEG precipitation method (PRISM™ Ready Reaction DyeDeoxy™ Terminator Cycle Sequencing Kit Protocols; ABI/Perkin Elmer).

10 The nucleotide sequence of both strands of the insert DNA was determined, using T7 primers [pBC KS(+) bases 601-623: TAAAACGACGGCCAGTGAGCGCG) and LacZ primers [pBC KS(+) bases 792-816: ATGACCATGATTACGCCAAGCGCGC) and protocols supplied with the PRISM™ sequencing kit (ABI/Perkin Elmer). Nonincorporated dye-terminator dideoxyribonucleotides were removed by passage through

15 Centri-Sep 100 columns (Princeton Separations, Inc., Adelphia, NJ) according to the manufacturer's instructions. The DNA sequence was obtained by analysis of the samples on an ABI Model 373A DNA Sequencer (ABI/Perkin Elmer). The DNA sequences of two

20 isolates, G24 and HB14, were found to be as illustrated in Figure 1.

This sequence illustrates the following features: 1) bases 1-20 represent one of the 64 possible sequences of the S4Psh degenerate oligonucleotides, ii) the sequence of amino acids 1-3

25 and 6-12 correspond exactly to that determined for the N-terminus of TcaC (disclosed as SEQ ID NO:2), iii) the fourth amino acid encoded is a cysteine residue rather than serine. This difference is encoded within the degeneracy for the serine codons (see above), iv) the fifth amino acid encoded is proline,

30 corresponding to the TcaC N-terminal sequence given as SEQ ID NO:2, v) bases 257-276 encode one of the 192 possible sequences designed into the degenerate pool, vi) the TGA termination codon introduced at bases 268-270 is the result of complementarity to the degeneracy built into the oligonucleotide pool at the

35 corresponding position, and does not indicate a shortened reading frame for the corresponding gene.

Labeling of a TcaC peptide gene-specific probe. DNA fragments corresponding to the above 276 bases were amplified (35

cycles) by PCR[®] in a 100 µl reaction volume, using 100 pmol each of P2Psh and P2.3.5R primers, 10 ng of plasmids GZ4 or HB14 as templates, 20 nmol each of dATP, dCTP, dGTP, and dTTP, 5 units of AmpliTaq[®] DNA polymerase, and 1X concentration of GeneAmp[®] buffer, under the same temperature regimes as described above. The amplification products were extracted from a 1% GTG[®] agarose gel by Qiaex kit and quantitated by fluorometry.

The extracted amplification products from plasmid HB14 template (approximately 400 ng) were split into five aliquots and labeled with ³²P-dCTP using the High Prime Labeling Mix (Boehringer Mannheim) according to the manufacturer's instructions. Nonincorporated radioisotope was removed by passage through NucTrap[®] Probe Purification Columns (Stratagene), according to the supplier's instructions. The specific activity of the labeled DNA product was determined by scintillation counting to be 3.11×10^8 dpm/µg. This labeled DNA was used to probe membranes prepared from 800 members of the genomic library.

Screening with a TcaC-peptide gene specific probe. The radiolabeled HB14 probe was boiled approximately 10 min, then added to "minimal hyb" solution. [Note: The "minimal hyb" method is taken from a CERES protocol; "Restriction Fragment Length Polymorphism Laboratory Manual version 4.0", sections 4-40 and 4-47; CERES/NPI, Salt Lake City, UT. NPI is now defunct, with its successors operating as Linkage Genetics]. "Minimal hyb" solution contains 10% w/v PEG (polyethylene glycol, M.W. approx. 8000), 7% w/v SDS; 0.6X SSC, 10 mM sodium phosphate buffer (from a 1M stock containing 95 g/l NaH₂PO₄·1H₂O and 84.5 g/l Na₂HPO₄·7H₂O), 5 mM EDTA, and 100 mg/ml denatured salmon sperm DNA. Membranes were blotted dry briefly then, without prehybridization, 5 strips of membrane were placed in each of 2 plastic boxes containing 75 ml of "minimal hyb" and 2.6 ng/ml of radiolabeled HB14 probe. These were incubated overnight with slow shaking (50 rpm) at 60°C. The filters were washed three times for approximately 10 min each at 25°C in "minimal hyb wash solution" (0.25X SSC, 0.2% SDS), followed by two 30-min washes with slow shaking at 60°C in the same solution. The filters were placed on paper covered with Saran Wrap[®] (Dow Brands, Indianapolis, IN) in a light-tight autoradiographic cassette and exposed to X-Omat X-ray film (Kodak, Rochester, NY) with two

DuPont Cronex Lightning-Plus C1 enhancers (Sigma Chemical Co., St. Louis, MO). for 4 hr at -70°C. Upon development (standard photographic procedures), significant signals were evident in both replicates amongst a high background of weaker, more irregular signals. The filters were again washed for about 4 hr at 68°C in "minimal hyb wash solution" and then placed again in the cassettes and film was exposed overnight at -70°C. Twelve possible positives were identified due to strong signals on both of the duplicate 96-well colony impressions. No signal was seen with negative control membranes (colonies of XL1 Blue MR cells containing pWE15), and a very strong signal was seen with positive control membranes (DH5 α cells containing the GZ4 isolate of the PCR product) that had been processed concurrently with the experimental samples.

The twelve putative hybridization-positive colonies were retrieved from the frozen 96-well library plates and grown overnight at 37°C on solid LB-Amp₁₀₀ medium. They were then patched (3/plate, plus three negative controls: XL1 Blue MR cells containing the pWE15 vector) onto solid LB-Amp₁₀₀. Two sets of membranes (Magna NT nylon, 0.45 micron) were prepared for hybridization. The first set was prepared by placing a filter directly onto the colonies on a patch plate, then removing it with adherent bacterial cells, and processing as below. Filters of the second set were placed on plates containing LB-Amp₁₀₀ medium, then inoculated by transferring cells from the patch plates onto the filters. After overnight growth at 37°C, the filters were removed from the plates and processed.

Bacterial cells on the filters were lysed and DNA denatured by placing each filter colony-side-up on a pool (1.0 ml) of 0.5 N NaOH in a plastic plate for 3 min. The filters were blotted dry on a paper towel, then the process was repeated with fresh 0.5 N NaOH. After blotting dry, the filters were neutralized by placing each on a 1.0 ml pool of 1 M Tris-HCl, pH 7.5 for 3 min, blotted dry, and reneutralised with fresh buffer. This was followed by two similar soakings (5 min each) on pools of 0.5 M Tris-HCl pH 7.5 plus 1.5 M NaCl. After blotting dry, the DNA was UV crosslinked to the filter (as above), and the filters were washed (25°C, 100 rpm) in about 100 ml of 3X SSC plus 0.1% (w/v) SDS (4 times, 30 min each with fresh solution for each wash). They were then placed in a minimal volume of prehybridization

solution (5X SSC plus 1% w/v each of Ficoll 400 (Pharmacia), polyvinylpyrrolidone (av. M.W. 360,000; Sigma) and bovine serum albumin Fraction V; (Sigma)) for 2 hr at 65°C, 50 rpm. The prehybridization solution was removed, and replaced with the HB14 ³²P-labeled probe that had been saved from the previous hybridization of the library membranes and which had been denatured at 95°C for 5 min. Hybridization was performed at 60°C for 16 hr with shaking at 50 rpm.

Following removal of the labeled probe solution, the membranes were washed 3 times at 25°C (50 rpm, 15 min) in 3X SSC (about 150 ml each wash). They were then washed for 3 hr at 68°C (50 rpm) in 0.25X SSC plus 0.2% SDS (minimal hyb wash solution), and exposed to X-ray film as described above for 1.5 hr at 25°C (no enhancer screens). This exposure revealed very strong hybridization signals to cosmid isolates 22G12, 25A10, 26A5, and 26B10, and a very weak signal with cosmid isolate 8B10. No signal was seen with the negative control (pWE15) colonies, and a very strong signal was seen with positive control membranes (DH5α cells containing the GZ4 isolate of the PCR product) that had been processed concurrently with the experimental samples.

Amplification of a specific genomic fragment of a *tcaB* gene.

Based on the N-terminal amino acid sequence determined for the purified TcaB_i peptide fraction (disclosed here as SEQ ID NO:3) a pool of degenerate oligonucleotides (pool P8F) was synthesized as described for peptide TcaC. The determined amino acid sequence and the corresponding degenerate DNA sequence are given below, where A, C, G, and T are the standard DNA bases, and I represents inosine:

30	Amino										
	Acid	Leu	Phe	Thr	Gln	Thr	Leu	Lys	Glu	Ala	Arg
35	P8F	5'	TTT	ACI	CA(A/G)	ACI	(C/T)TI	AAA	GAA	GCI	(A/C)G 3'
			(C/T)TI								

Another set of degenerate oligonucleotides was synthesized (pool P8.108.3R), representing the complement of the coding strand for the determined amino acid sequence of the TcaB_i-PT108 internal peptide (disclosed herein as SEQ ID NO:20):

40	Amino							
	Acid	Met	Tyr	Tyr	Ile	Gln	Ala	Gln

Codons ATG TA(T/C) TA(T/C) AT(T/C/A) CA(A/G) GC(A/C/G/T) CA(A/G) CA(A/G)
 P8.108.3R 3' AT(A/G) AT(A/G) TA(A/G/T) GT(T/C) CGI GT(T/C) GT 5'
 TAC

5

These oligonucleotides were used as primers for PCR[®] using HotStart 50 Tubes[™] (Molecular Bio-Products, Inc., San Diego, CA) to amplify a specific DNA fragment from genomic DNA prepared from *Photorhabdus* strain W-14 (see above). A typical reaction (50 μ l) contained (bottom layer) 25 pmol of each primer pool P8F and P8.108.3R, with 2 nmol each of dATP, dCTP, dGTP, and dTTP, in 1X GeneAmp[®] PCR buffer, and (top layer) 230 ng of genomic template DNA, 8 nmol each of dATP, dCTP, dGTP, and dTTP, and 2.5 units of AmpliTaq[®] DNA polymerase, in 1X GeneAmp[®] PCR buffer.

Amplifications were performed by 35 cycles as described for the TcaC peptide. Amplification products were analyzed by electrophoresis through 0.7% w/v SeaKem[®] LE agarose (FMC) in TEA buffer. A specific product of estimated size 1600 bp was observed.

20

Four such reactions were pooled, and the amplified DNA was extracted from a 1.0% SeaKem[®] LE gel by Qiaex kit as described for the TcaC peptide. The extracted DNA was used directly as the template for sequence determination (PRISM[™] Sequencing Kit) using the P8F and P8.108.3R primer pools. Each reaction contained about 100 ng template DNA and 25 pmol of one primer pool, and was processed according to standard protocols as described for the TcaC peptide. An analysis of the sequence derived from extension of the P8F primers revealed the short DNA sequence (and encoded amino acid sequence):

30

GAT GCA TTG NTT GCT
 Asp Ala Leu (Val) Ala

which corresponds to a portion of the N-terminal peptide sequence disclosed as SEQ ID NO:3 (TcaB_i).

35

Labeling of a TcaB_i-peptide gene-specific probe.

Approximately 50 ng of gel-purified TcaB_i DNA fragment was labeled with ³²P-dCTP as described above, and nonincorporated radioisotopes were removed by passage through a NICK Column[®] (Pharmacia). The specific activity of the labelled DNA was determined to be 6 x 10⁹ dpm/ μ g. This labeled DNA was used to

probe colony membranes prepared from members of the genomic library that had hybridized to the TcaC-peptide specific probe.

The membranes containing the 12 colonies identified in the TcaC-probe library screen (see above) were stripped of
5 radioactive TcaC-specific label by boiling twice for approximately 30 min each time in 1 liter of 0.1X SSC plus 0.1 % SDS. Removal of radiolabel was checked with a 6 hr film exposure. The stripped membranes were then incubated with the TcaB_i peptide-specific probe prepared above. The labeled DNA was
10 denatured by boiling for 10 min, and then added to the filters that had been incubated for 1 hr in 100 ml of "minimal hyb" solution at 60°C. After overnight hybridization at this temperature, the probe solution was removed, and the filters were washed as follows (all in 0.3X SSC plus 0.1% SDS): once for 5 min
15 at 25°C, once for 1 hr at 60°C in fresh solution, and once for 1 hr at 63°C in fresh solution. After 1.5 hr exposure to X-ray film by standard procedures, 4 strongly-hybridizing colonies were observed. These were, as with the TcaC-specific probe, isolates 22G12, 25A10, 26A5, and 26B10.

20 The same TcaB_i probe solution was diluted with an equal volume (about 100 ml) of "minimal hyb" solution, and then used to screen the membranes containing the 800 members of the genomic library. After hybridization, washing, and exposure to X-ray film as described above, only the four cosmid clones 22G12,
25 25A10, 26A5, and 26B10, were found to hybridize strongly to this probe.

ISOLATION OF SUBCLONES CONTAINING GENES ENCODING TcaC AND TcaB_i PEPTIDES, AND DETERMINATION OF DNA BASE SEQUENCE THEREOF:

30 Three hybridization-positive cosmids in strain XL1 Blue MR were grown with shaking overnight (200 rpm) at 30°C in 100 ml TB-Amp^r. After harvesting the cells by centrifugation, cosmid DNA was prepared using a commercially available kit (BIGprep™, 5 Prime 3 Prime, Inc., Boulder, CO), following the manufacturer's
35 protocols. Only one cosmid, 26A5, was successfully isolated by this procedure. When digested with restriction enzyme EcoR 1 (NEB) and analyzed by gel electrophoresis, fragments of approximate sizes 14, 10, 8 (vector), 5, 3.3, 2.9, and 1.5 kbp were detected. A second attempt to isolate cosmid DNA from the
40 same three strains (8 ml cultures; TB-Amp^r, 30°C) utilized a

boiling miniprep method (Evans G. and G. Wahl., 1987, "Cosmid vectors for genomic walking and rapid restriction mapping." in Guide to Molecular Cloning Techniques. Meth. Enzymology, vol. 152, S. Berger and A. Kimmel, eds., pgs. 604-610). Only one
5 cosmid, 25A10, was successfully isolated by this method. When digested with restriction enzyme EcoR 1 (NEB) and analyzed by gel electrophoresis, this cosmid showed a fragmentation pattern identical to that previously seen with cosmid 26A5.

A 0.15 µg sample of 26A5 cosmid DNA was used to transform 50
10 ml of *E. coli* DH5α cells (Gibco BRL), by the supplier's protocols. A single colony isolate of that strain was inoculated into 4 ml of TB-Amp^r, and grown for 8 hr at 37°C. Chloramphenicol was added to a final concentration of 225 µg/ml, incubation was continued for another 24 hr, then cells were
15 harvested by centrifugation and frozen at -20°C. Isolation of the 26A5 cosmid DNA was by a standard alkaline lysis miniprep (Maniatis et al., op. cit., p. 382), modified by increasing all volumes by 50% and with stirring or gentle mixing, rather than vortexing, at every step. After washing the DNA pellet in 70%
20 ethanol, it was dissolved in TE containing 25 µg/ml ribonuclease A (Boehringer Mannheim).

Identification of EcoR 1 fragments hybridizing to GZ4-
derived and TcaBi₁- probes. Approximately 0.4 µg of cosmid 25A10
25 (from XL1 Blue MR cells) and about 0.5 µg of cosmid 26A5 (from chloramphenicol-amplified DH5α cells) were each digested with about 15 units of EcoR 1 (NEB) for 85 min, frozen overnight, then heated at 65°C for five min, and electrophoresed in a 0.7% agarose gel (Seakem[®] LE, 1X TEA, 80 volts, 90 min). The DNA was
30 stained with ethidium bromide as described above, and photographed under ultraviolet light. The EcoR 1 digest of cosmid 25A10 was a complete digestion, but the sample of cosmid 26A5 was only partially digested under these conditions. The agarose gel containing the DNA fragments was subjected to
35 depurination, denaturation and neutralization, followed by Southern blotting onto a Magna NT nylon membrane, using a high salt (20X SSC) protocol, all as described in section 2.9 of Ausubel et al. (CPMB, op. cit.). The transferred DNA was then UV-crosslinked to the nylon membrane as before.

An TcaC-peptide specific DNA fragment corresponding to the insert of plasmid isolate GZ4 was amplified by PCR* in a 100 ml reaction volume as described previously above. The amplification products from three such reactions were pooled and were extracted from a 1% GTG* agarose gel by Qiaex kit, as described above, and quantitated by fluorometry. The gel-purified DNA (100 ng) was labeled with ³²P-dCTP using the High Prime Labeling Mix (Boehringer Mannheim) as described above, to a specific activity of 6.34×10^8 dpm/ μ g.

10 The ³²P-labeled GZ4 probe was boiled 10 min, then added to "minimal hyb" buffer (at 1 ng/ml), and the Southern blot membrane containing the digested cosmid DNA fragments was added, and incubated for 4 hr at 60°C with gentle shaking at 50 rpm. The membrane was then washed 3 times at 25°C for about 5 min each
15 (minimal hyb wash solution), followed by two washes for 10 min each at 60°C. The blot was exposed to film (with enhancer screens) for about 30 min at -70°C. The GZ4 probe hybridized strongly to the 5.0 kbp (apparent size) EcoR 1 fragment of both these two cosmids, 26A5 and 25A10.

20 The membrane was stripped of radioactivity by boiling for about 30 min in 0.1X SSC plus 0.1 % SDS, and absence of radiolabel was checked by exposure to film. It was then hybridized at 60°C for 3.5 hours with the (denatured) TcaB_i probe in "minimal hyb" buffer previously used for screening the colony
25 membranes (above), washed as described previously, and exposed to film for 40 min at -70°C with two enhancer screens. With both cosmids, the TcaB_i probe hybridized lightly with the about 5.0 kbp EcoR 1 fragment, and strongly with a fragment of approximately 2.9 kbp.

30 The sample of cosmid 26A5 DNA previously described, (from DH5 α cells) was used as the source of DNA from which to subclone the bands of interest. This DNA (2.5 μ g) was digested with about 3 units of EcoR 1 (NEB) in a total volume of 30 μ l for 1.5 hr, to give a partial digest, as confirmed by gel electrophoresis. Ten
35 μ g of pBC KS (+) DNA (Stratagene) were digested for 1.5 hr with 20 units of EcoR 1 in a total volume of 20 μ l, leading to total digestion as confirmed by electrophoresis. Both EcoR 1-cut DNA preparations were diluted to 50 μ l with water, to each an equal volume of PCI was added, the suspension was gently mixed, spun in

a microcentrifuge and the aqueous supernatant was collected. DNA was precipitated by 150 μ l ethanol, and the mixture was placed at -20°C overnight. Following centrifugation and drying, the EcoR 1-digested pBC KS (+) was dissolved in 100 μ l TE; the partially
5 digested 26A5 was dissolved in 20 μ l TE. DNA recovery was checked by fluorometry.

In separate reactions, approximately 60 ng of EcoR 1-digested pBC KS(+) DNA was ligated with approximately 180 ng or 270 ng of partially digested cosmid 26A5 DNA. Ligations were
10 carried out in a volume of 20 μ l at 15°C for 5 hr, using T4 ligase and buffer from New England BioLabs. The ligation mixture, diluted to 100 μ l with sterile TE, was used to transform frozen, competent DH5 α cells (Gibco BRL) according to the supplier's instructions. Varying amounts (25-200 μ l) of the
15 transformed cells were plated on freshly prepared solid LB-Cam₃s medium with 1 mM IPTG and 50 mg/l X-gal. Plates were incubated at 37°C about 20 hr, then chilled in the dark for approximately 3 hr to intensify color for insert selection. White colonies were picked onto patch plates of the same composition and incubated
20 overnight at 37°C.

Two colony lifts of each of the selected patch plates were prepared as follows. After picking white colonies to fresh plates, round Magna NT nylon membranes were pressed onto the patch plates, the membrane was lifted off, and subjected to
25 denaturation, neutralization and UV crosslinking as described above for the library colony membranes. The crosslinked colony lifts were vigorously washed, including gently wiping off the excess cell debris with a tissue. One set was hybridized with the GZ4(TcaC) probe solution described earlier, and the other set
30 was hybridized with the TcaB_i probe solution described earlier, according to the 'minimal hyb' protocol, followed by washing and film exposure as described for the library colony membranes.

Colonies showing hybridization signals either only with the GZ4 probe, with both GZ4 and TcaB_i probes, or only with the TcaB_i
35 probe, were selected for further work and cells were streaked for single colony isolation onto LB-Cam₃s media with IPTG and X-gal as before. Approximately 35 single colonies, from 16 different isolates, were picked into liquid LB-Cam₃s media and grown

overnight at 37°C; the cells were collected by centrifugation and plasmid DNA was isolated by a standard alkaline lysis miniprep according to Maniatis et al. (op. cit. p. 368). DNA pellets were dissolved in TE + 25 µg/ml ribonuclease A and DNA concentration was determined by fluorometry. The EcoR 1 digestion pattern was analyzed by gel electrophoresis. The following isolates were picked as useful. Isolate A17.2 contains religated pBC KS(+) only and was used for a (negative) control. Isolates D38.3 and C44.1 each contain only the 2.9 kbp, TcaB_i -hybridizing EcoR 1 fragment inserted into pBC KS(+). These plasmids, named pDAB2000 and pDAB2001, respectively, are illustrated in Fig. 2.

Isolate A35.3 contains only the approximately 5 kbp, GZ4)-hybridizing EcoR 1 fragment, inserted into pBC KS(+). This plasmid was named pDAB2002 (also Fig. 2). These isolates provided templates for DNA sequencing.

Plasmids pDAB2000 and pDAB2001 were prepared using the BIGprep™ kit as before. Cultures (30 ml) were grown overnight in TB-Cam₃₅ to an OD₆₀₀ of 2, then plasmid was isolated according to the manufacturer's directions. DNA pellets were redissolved in 100 µl TE each, and sample integrity was checked by EcoR 1 digestion and gel electrophoretic analysis.

Sequencing reactions were run in duplicate, with one replicate using as template pDAB2000 DNA, and the other replicate using as template pDAB2001 DNA. The reactions were carried out using the dideoxy dye terminator cycle sequencing method, as described above for the sequencing of the GZ4/HB14 DNAs. Initial sequencing runs utilized as primers the LacZ and T7 primers described above, plus primers based on the determined sequence of the TcaB_i PCR amplification product (TH1 = ATTGCAGACTGCCAATCGCTTCGG, TH12 = GAGAGTATCCAGACCGCGGATGATCTG).

After alignment and editing of each sequencing output, each was truncated to between 250 to 350 bases, depending on the integrity of the chromatographic data as interpreted by the Perkin Elmer Applied Biosystems Division SeqEd 675 software. Subsequent sequencing "steps" were made by selecting appropriate sequence for new primers. With a few exceptions, primers (synthesized as described above) were 24 bases in length with a 50% G+C composition. Sequencing by this method was carried out on both strands of the approximately 2.9 kbp EcoR 1 fragment.

To further serve as template for DNA sequencing, plasmid DNA from isolate pDAB2002 was prepared by BIGprep™ kit. Sequencing reactions were performed and analyzed as described above.

Initially, a T3 primer (pBS SK (+) bases 774-796:

- 5 CGCGCAATTAACCCTCACTAAAG) and a T7 primer (pBS KS (+) bases 521-643: GCGCGTAATACGACTCACTATAG) were used to prime the sequencing reactions from the flanking vector sequences, reading into the insert DNA. Another set of primers, (GZ4F: GTATCGATTACAACGCTGTCACTTCCC; TH13: GGGAAGTGACAGCGTTGTAATCGATAC; TH14: ATGTTGGGTGCGTCGGCTAATGGACATAAC; and LW1-204: GGGAAGTGACAGCGTTGTAATCGATAC) was made to prime from internal sequences, which were determined previously by degenerate oligonucleotide-mediated sequencing of subcloned TcaC-peptide PCR products. From the data generated during the initial rounds of sequencing, new sets of primers were designed and used to walk the entire length of the ~5 kbp fragment. A total of 55 oligo primers was used, enabling the identification of 4832 total bp of contiguous sequence.

- When the DNA sequence of the EcoR 1 fragment insert of pDAB2002 is combined with part of the determined sequence of the pDAB2000/pDAB2001 isolates, a total contiguous sequence of 6005 bp was generated (disclosed herein as SEQ ID NO:25). When long open reading frames were translated into the corresponding amino acids, the sequence clearly shows the TcaB_i N-terminal peptide (disclosed as SEQ ID NO:3), encoded by bases 19-75, immediately following a methionine residue (start of translation). Upstream lies a potential ribosome binding site (bases 1-9), and downstream, at bases 166-228 is encoded the TcaB_i-PT158 internal peptide (disclosed herein as SEQ ID NO:19). Further downstream, in the same reading frame, at bases 1738-1773, exists a sequence encoding the TcaB_i-PT108 internal peptide (disclosed herein as SEQ ID NO:20). Also in the same reading frame, at bases 1897-1923, is encoded the TcaB_{ii} N-terminal peptide (disclosed herein as SEQ ID NO:5), and the reading frame continues uninterrupted to a translation termination codon at nucleotides 3586-3588.

The lack of an in-frame stop codon between the end of the sequence encoding TcaB_i-PT108 and the start of the TcaB_{ii} encoding region, and the lack of a discernible ribosome binding site immediately upstream of the TcaB_{ii} coding region, indicate that

peptides TcaB_{ii} and TcaB_i are encoded by a single open reading frame of 3567 bp beginning at base pair 16 in SEQ ID NO:25), and are most likely derived from a single primary gene product of 1189 amino acids (131,586 Daltons; disclosed herein as SEQ ID NO:26) by post-translational cleavage. If the amino acid immediately preceding the TcaB_{ii} N-terminal peptide represents the C-terminal amino acid of peptide TcaB_i, then the predicted mass of TcaB_{ii} (627 amino acids) is 70,814 Daltons (disclosed herein as SEQ ID NO:28), somewhat higher than the size observed by SDS-PAGE (68 kDa). This peptide would be encoded by a contiguous stretch of 1881 base pairs (disclosed herein as SEQ ID NO:27). It is thought that the native C-terminus of TcaB_i lies somewhat closer to the C-terminus of TcaB_i-PT108. The molecular mass of PT108 [3.438 kDa; determined during N-terminal amino acid sequence analysis of this peptide] predicts a size of 30 amino acids. Using the size of this peptide to designate the C-terminus of the TcaB_i coding region [Glu at position 604 of SEQ ID NO:28], the derived size of TcaB_i is determined to be 604 amino acids or 68,463 Daltons, more in agreement with experimental observations.

Translation of the TcaB_{ii} peptide coding region of 1686 base pairs (disclosed herein as SEQ ID NO:29) yields a protein of 562 amino acids (disclosed herein as SEQ ID NO:30) with predicted mass of 60,789 Daltons, which corresponds well with the observed 61 kDa.

A potential ribosome binding site (bases 3633-3638) is found 48 bp downstream of the stop codon for the *tcaB* open reading frame. At bases 3645-3677 is found a sequence encoding the N-terminus of peptide TcaC, (disclosed as SEQ ID NO.2). The open reading frame initiated by this N-terminal peptide continues uninterrupted to base 6005 (2361 base pairs, disclosed herein as the first 2361 base pairs of SEQ ID NO.31). A gene (*tcaC*) encoding the entire TcaC peptide, (apparent size ~165 kDa; ~1500 amino acids), would comprise about 4500 bp.

Another isolate containing cloned EcoR 1 fragments of cosmid 26A5, E20.6, was also identified by its homology to the previously mentioned GZ4 and TcaB_i probes. Agarose gel analysis of EcoR 1 digests of the DNA of the plasmid harbored by this strain (pDAB2004, Fig. 2), revealed insert fragments of estimated

sizes 2.9, 5, and 3.3 kbp. DNA sequence analysis initiated from primers designed from the sequence of plasmid pDAB2002 revealed that the 3.3 kbp EcoR 1 fragment of pDAB2004 lies adjacent to the 5 kbp EcoR 1 fragment represented in pDAB2002. The 2361 base pair open reading frame discovered in pDAB2002 continues uninterrupted for another 2094 bases in pDAB2004 [disclosed herein as base pairs 2362 to 4458 of SEQ ID NO:31]. DNA sequence analysis using the parent cosmid 26A5 DNA as template confirmed the continuity of the open reading frame. Altogether, the open reading frame (TcaC SEQ ID NO:31) comprises 4455 base pairs, and encodes a protein (TcaC) of 1485 amino acids [disclosed herein as SEQ ID NO:32]. The calculated molecular size of 166,214 Daltons is consistent with the estimated size of the TcaC peptide (165 kDa), and the derived amino acid sequence matches exactly that disclosed for the TcaC N-terminal sequence [SEQ ID NO:2].

The lack of an amino acid sequence corresponding to SEQ ID NO:17; used to design the degenerate oligonucleotide primer pool in the discovered sequence indicates that the generation of the PCR® products found in isolates GZ4 and HB14, which were used as probes in the initial library screen, were fortuitously generated by reverse-strand priming by one of the primers in the degenerate pool. Further, the derived protein sequence does not include the internal fragment disclosed herein as SEQ ID NO:18. These sequences reveal that plasmid pDAB2004 contains the complete coding region for the TcaC peptide.

Example 9

Screening of the *Photorhabdus* genomic library for genes encoding the TcbA_{ii} peptide

30

This example describes a method used to identify DNA clones that contain the TcbA_{ii} peptide-encoding genes, the isolation of the gene, and the determination of its partial DNA base sequence.

35

Primers and PCR reactions

The TcbA_{ii} polypeptide of the insect active preparation is ~206 kDa. The amino acid sequence of the N-terminus of this peptide is disclosed as SEQ ID NO:1. Four pools of degenerate oligonucleotide primers ("Forward primers": TH-4, TH-5, TH-6, and

TH-7) were synthesized to encode a portion of this amino acid sequence, as described in Example 8, and are shown below.

Table 11

5	Amino Acid	Phe	Ile	Gln	Gly	Tyr	Ser	Asp	Leu	Phe
	TH-4	5'-TT(T/C)	ATI	CA(A/G)	GGI	TA(T/C)	TCI	GA(T/C)	CTI	TT-3'
	TH-5	5'-TT(T/C)	ATI	CA(A/G)	GGI	TA(T/C)	AG(T/C)	GA(T/C)	CTI	TT-3'
	TH-6	5'-TT(T/C)	ATI	CA(A/G)	GGI	TA(T/C)	TCI	GA(T/C)	TT(A/G)	TT-3'
10	TH-7	5'-TT(T/C)	ATI	CA(A/G)	GGI	TA(T/C)	AG(T/C)	GA(T/C)	TT(A/G)	TT-3'

In addition, a primary ("a") and a secondary ("b") sequence of an internal peptide preparation (TcbA_{ii}-PT81) have been determined and are disclosed herein as SEQ ID No:23 and SEQ ID No:24, respectively. Four pools of degenerate oligonucleotides ("Reverse Primers": TH-8, TH-9, TH-10 and TH-11) were similarly designed and synthesized to encode the reverse complement of sequences that encode a portion of the peptide of SEQ ID NO:23, as shown below.

Table 12

Amino Acid	Thr	Tyr	Leu	Thr	Ser	Phe	Glu	Gln	Val	Ala	Asn
TH-8	3'TGI	AT(A/G)	GAI	TGI	AGI	AA(A/G)	CT(T/C)	GT(T/C)	CAI	CGI	TT(G/A)-5'
TH-9	3'TGI	AT(A/G)	TT(A/G)	TGI	AGI	AA(A/G)	CT(T/C)	GT(T/C)	CAI	CGI	TT(G/A)-5'
TH-10	3'TGI	AT(A/G)	GAI	TGI	TC(G/A)	AA(A/G)	CT(T/C)	GT(T/C)	CAI	CGI	TT(G/A)-5'
TH-11	3'TGI	AT(A/G)	TT(A/G)	TGI	TC(G/A)	AA(A/G)	CT(T/C)	GT(T/C)	CAI	CGI	TT(G/A)-5'

Sets of these primers were used in PCR[®] reactions to amplify TcbA_{ii}- encoding gene fragments from the genomic *Photorhabdus luminescens* W-14 DNA prepared in Example 6. All PCR[®] reactions were run with the "Hot Start" technique using AmpliWax™ gems and other Perkin Elmer reagents and protocols. Typically, a mixture (total volume 11 µl) of MgCl₂, dNTP's, 10X GeneAmp[®] PCR Buffer II, and the primers were added to tubes containing a single wax bead. [10X GeneAmp[®] PCR Buffer II is composed of 100 mM Tris-HCl, pH 8.3; and 500 mM KCl.] The tubes were heated to 80°C for 2 minutes and allowed to cool. To the top of the wax seals, a solution containing 10X GeneAmp[®] PCR Buffer II, DNA template, and AmpliTaq[®] DNA polymerase were added. Following melting of the wax seal and mixing of components by thermal cycling, final reaction conditions (volume of 50 µl) were: 10 mM Tris-HCl, pH 8.3; 50 mM KCl; 2.5 mM MgCl₂; 200 µM each in dATP, dCTP, dGTP, dTTP; 1.25 mM in a single Forward primer pool; 1.25 µM in a single Reverse primer pool, 1.25 units of AmpliTaq[®] DNA polymerase, and 170 ng of template DNA.

20 The reactions were placed in a thermocycler (as in Example 8) and run with the following program:

Table 13

Temperature	Time	Cycle Repetition
94°C	2 minutes	1X
94°C	15 seconds	
55-65°C	30 seconds	30X
72°C	1 minute	
72°C	7 minutes	1X
15°C	Constant	

A series of amplifications was run at three different annealing temperatures (55°, 60°, 65° C) using the degenerate primer pools. Reactions with annealing at 65°C had no amplification products visible following agarose gel electrophoresis. Reactions having a 60°C annealing regime and containing primers TH-5+TH-10 produced an amplification product that had a mobility corresponding to 2.9 kbp. A lesser amount of the 2.9 kbp product was produced under these conditions with primers TH-7+TH-10. When reactions were annealed at 55°C, these primer pairs produced more of the 2.9 kbp product, and this product was also produced by primer pairs TH-5+TH-8 and TH-5+TH-11. Additional very faint 2.9 kbp bands were seen in lanes containing amplification products from primer pairs TH-7 plus TH-8, TH-9, TH-10, or TH-11.

To obtain sufficient PCR amplification product for cloning and DNA sequence determination, 10 separate PCR reactions were set up using the primers TH-5+TH-10, and were run using the above conditions with a 55°C annealing temperature. All reactions were pooled and the 2.9 kbp product was purified by Qiaex extraction from an agarose gel as described above.

Additional sequences determined for TcbA_{ii} internal peptides are disclosed herein as SEQ ID NO:21 and SEQ ID NO:22. As before, degenerate oligonucleotides (Reverse primers TH-17 and TH-18) were made corresponding to the reverse complement of sequences that encode a portion of the amino acid sequence of these peptides.

Table 14

From SEQ ID NO:21

Amino Acid	Met	Glu	Thr	Gln	Asn	Ile	Gln	Glu	Pro
TH-17	3'-TAC	CTT/C	TGI	GTT/C	TTA/G	TAI	GTT/C	GTT/C	GG-5'

Table 15

From SEQ ID NO:22

Amino Acid	Asn	Pro	Ile	Asn	Ile	Asn	Thr	Gly	Ile	Asp
TH-18	3'-TT(A/G)	GGI	TAI	TT(A/G)	TAI	TT(A?G)	TGI	CCI	TAI	CT(A/G)-5'

Degenerate oligonucleotides TH-18 and TH-17 were used in an amplification experiment with *Photorhabdus luminescens* W-14 DNA as template and primers TH-4, TH-5, TH-6, or TH-7 as the 5'-(Forward) primers. These reactions amplified products of approximately 4 kbp and 4.5 kbp, respectively. These DNAs were transferred from agarose gels to nylon membranes and hybridized with a ³²P-labeled probe (as described above) prepared from the 2.9 kbp product amplified by the TH-5+TH10 primer pair. Both the 4 kbp and the 4.5 kbp amplification products hybridized strongly to the 2.9 kbp probe. These results were used to construct a map ordering the TcbAii internal peptide sequences as shown in Fig. 3. Approximate distances between the primers are shown in nucleotides in Fig. 3.

15 DNA Sequence of the 2.9 kbp TcbAii-encoding fragment

Approximately 200 ng of the purified 2.9 kbp fragment (prepared above) was precipitated with ethanol and dissolved in 17 ml of water. One-half of this was used as sequencing template with 25 pmol of the TH-5 pool as primers, the other half was used as template for TH-10 priming. Sequencing reactions were as given in Example 8. No reliable sequence was produced using the TH-10 primer pool; however, reactions with TH-5 primer pool produced the sequence disclosed below:

```

25      1  AATCGTGTTG ATCCCTATGC CGNGCCGGGT TCGGTGGAAT CGATGTCCTC ACCGGGGGTT
      51  TATTNGAGGG ANTNGTCCCG TGAGGCCAAA AANTGGAATG AAAGAAGTTC AATTNTTAC
      121  CTAGATAAAC GTCGCCCGGN TTTAGAAAGN TTANTGNTCA GCCAGAAAAT TTTGGTTGAG
      181  GAAATTCCAC CGNTGGTTCT CTCTATTGAT TNGGGCCTGG CCGGGTTCGA ANNAAAACNA
      241  GGAAATNCAC AAGTTGAGGT GATGGNTTTG THGCNANCTT NTCGTTTAGG TGGGGAGAAA
      301  CCTTNTCANC ACGNTTNTGA AACTGTCCGG GAAATCGTCC ATGANCGTGA NCCAGGNTTN
30      361  CGCCATTGG

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Based on this sequence, a sequencing primer (TH-21, 5'-CCGGGCGACGTTTATCTAGG-3') was designed to reverse complement bases 120-139, and initiate polymerization towards the 5' end (i.e., TH-5 end) of the gel-purified 2.9 kbp TcbAii-encoding PCR fragment. The determined sequence is shown below, and is compared to the biochemically determined N-terminal peptide sequence of TcbAii SEQ ID NO:1.

TcbAii 2.9 kbp PCR fragment Sequence Confirmation

[Underlined amino acids = encoded by degenerate oligonucleotides]

5 SEQ ID NO:1 F I Q G Y S D L F G - - A
 2.9 kbp seq GC ATG CAG GGG TAT AGT GAC CTG TTT GGT AAT CGT GCT
 M Q G Y S D L F G N R A

10 From the homology of the derived amino acid sequence to the biochemically determined one, it is clear that the 2.9 kbp PCR fragment represents the *TcbA* coding region. This 2.9 kbp fragment was then used as a hybridization probe to screen the *Photorhabdus* W-14 genomic library prepared in Example 8 for cosmids containing the *TcbAii*-encoding gene.

15

Screening the *Photorhabdus* cosmid library

The 2.9 kb gel-purified PCR fragment was labeled with ³²P using the Boehringer Mannheim High Prime labeling kit as described in Example 8. Filters containing remnants of approximately 800 colonies from the cosmid library were screened as described previously (Example 8), and positive clones were streaked for isolated colonies and rescreened. Three clones (8A11, 25G8, and 26D1) gave positive results through several screening and characterization steps. No hybridization of the *TcbAii*-specific probe was ever observed with any of the four cosmids identified in Example 8, and which contain the *tcaB* and *tcaC* genes. DNA from cosmids 8A11, 25G8, and 26D1 was digested with restriction enzymes Bgl 2, EcoR 1 or Hind 3 (either alone or in combination with one another), and the fragments were separated on an agarose gel and transferred to a nylon membrane as described in Example 8. The membrane was hybridized with ³²P-labeled probe prepared from the 4.5 kbp fragment (generated by amplification of *Photorhabdus* genomic DNA with primers TH-5+TH-17). The patterns generated from cosmid DNAs 8A11 and 26D1 were identical to those generated with similarly-cut genomic DNA on the same membrane. It is concluded that cosmids 8A11 and 26D1 are accurate representations of the genomic *TcbAii* encoding locus. However, cosmid 25G8 has a single Bgl 2 fragment which is slightly larger than the genomic DNA. This may result from positioning of the insert within the vector.

DNA sequence of the tcbA-encoding gene

The membrane hybridization analysis of cosmid 26D1 revealed that the 4.5 kbp probe hybridized to a single large EcoR I fragment (greater than 9 kbp). This fragment was gel purified and ligated into the EcoR I site of pBC KS (+) as described in Example 8, to generate plasmid pBC-S1/R1. The partial DNA sequence of the insert DNA of this plasmid was determined by "primer walking" from the flanking vector sequence, using procedures described in Example 8. Further sequence was generated by extension from new oligonucleotides designed from the previously determined sequence. When compared to the determined DNA sequence for the tcbA gene identified by other methods (disclosed herein as SEQ ID NO:11 as described in Example 12 below), complete homology was found to nucleotides 1-272, 319-826, 2578-3036, and 3068-3540 (total bases = 1712). It was concluded that both approaches can be used to identify DNA fragments encoding the TcbA_{ij} peptide.

Analysis of the derived amino acid sequence of the tcbA gene.

The sequence of the DNA fragment identified as SEQ ID NO:11 encodes a protein whose derived amino acid sequence is disclosed herein as SEQ ID NO:12. Several features verify the identity of the gene as that encoding the TcbA_{ij} protein. The TcbA_{ij} N-terminal peptide (SEQ ID NO:1; Phe Ile Gln Gly Tyr Ser Asp Leu Phe Gly Asn Arg Ala) is encoded as amino acids 88-100. The TcbA_{ij} internal peptide TcbA_{ij}-PT81(a) (SEQ ID NO:23) is encoded as amino acids 1065-1077, and TcbA_{ij}-PT81(b) (SEQ ID NO:24) is encoded as amino acids 1571-1592. Further, the internal peptide TcbA_{ij}-PT56 (SEQ ID NO:22) is encoded as amino acids 1474-1488, and the internal peptide TcbA_{ij}-PT103 (SEQ ID NO:24) is encoded as amino acids 1614-1639. It is obvious that this gene is an authentic clone encoding the TcbA_{ij} peptide as isolated from insecticidal protein preparations of *Photobacterium luminescens* strain W-14.

The protein isolated as peptide TcbA_{ij} is derived from cleavage of a longer peptide. Evidence for this is provided by the fact that the nucleotides encoding the TcbA_{ij} N-terminal peptide SEQ ID NO:1 are preceded by 261 bases (encoding 87 N-terminal-proximal amino acids) of a longer open reading frame (SEQ ID NO:11). This reading frame begins with nucleotides that encode the amino acid sequence Met Gln Asn Ser

Leu, which corresponds to the N-terminal sequence of the large peptide TcbA, and is disclosed herein as SEQ ID NO:15. It is thought that TcbA is the precursor protein for TcbA_{ii}.

5 Relationship of tcbA, tcaB and tcaC genes.

The tcaB and tcaC genes are closely linked and may be transcribed as a single mRNA (Example 8). The tcbA gene is borne on cosmids that apparently do not overlap the ones harboring the tcaB and tcaC cluster, since the respective genomic library
10 screens identified different cosmids. However, comparison of the amino sequences encoded by the tcaB and tcaC genes with the tcbA gene reveals a substantial degree of homology. The amino acid conservation (Protein Alignment Mode of MacVector™ Sequence
15 Analysis Software, scoring matrix pam250, hash value = 2; Kodak Scientific Imaging Systems, Rochester, NY) is shown in Fig. 4. On the score line of each panel in Fig. 4, up carats (^) indicate homology or conservative amino acid changes, and down carats (v) indicate nonhomology.

This analysis shows that the amino acid sequence of the TcbA
20 peptide from residues 1739 to 1894 is highly homologous to amino acids 441 to 603 of the TcaB_i peptide (162 of the total 627 amino acids of P8; SEQ ID NO:28). In addition, the sequence of TcbA amino acids 1932 to 2459 is highly homologous to amino acids 12 to 531 of peptide TcaB_{ii} (520 of the total 562 amino acids; SEQ
25 ID NO:30). Considering that the TcbA peptide (SEQ ID NO:12) comprises 2505 amino acids, a total of 684 amino acids (27%) at the C-proximal end of it is homologous to the TcaB_i or TcaB_{ii} peptides, and the homologies are arranged colinear to the arrangement of the putative TcaB preprotein (SEQ ID NO:26). A
30 sizeable gap in the TcbA homology coincides with the junction between the TcaB_i and TcaB_{ii} portions of the TcaB preprotein. Clearly the TcbA and TcaB gene products are evolutionarily related, and it is proposed that they share some common
35 function(s) in *Photorhabdus*.

Example 10Characterization of zinc-metalloproteases in *Photorhabdus* Broth:
Protease Inhibition, Classification, and Purification

5 Protease Inhibition and Classification Assays: Protease assays were performed using FITC-casein dissolved in water as substrate (0.08% final assay concentration). Proteolysis reactions were performed at 25°C for 1 h in the appropriate buffer with 25 μ l of *Photorhabdus* broth (150 μ l total reaction
10 volume). Samples were also assayed in the presence and absence of dithiothreitol. After incubation, an equal volume of 12% trichloroacetic acid was added to precipitate undigested protein. Following precipitation for 0.5 h and subsequent centrifugation, 100 μ l of the supernatant was placed into a 96-well microtiter
15 plate and the pH of the solution was adjusted by addition of an equal volume of 4N NaOH. Proteolysis was then quantitated using a Fluoroskan II fluorometric plate reader at excitation and emission wavelengths of 485 and 538 nm, respectively. Protease activity was tested over a range from pH 5.0-10.0 in 0.5 units
20 increments. The following buffers were used at 50 mM final concentration: sodium acetate (pH 5.0 - 6.5); Tris-HCL (pH 7.0 - 8.0); and bis-Tris propane (pH 8.5-10.0). To identify the class of protease(s) observed, crude broth was treated with a variety of protease inhibitors (0.5 μ g/ μ l final concentration) and then
25 examined for protease activity at pH 8.0 using the substrate described above. The protease inhibitors used included E-64 (L-trans-exposysaccinylleucylamido[4-, -guanidino]-butane), 3,4 dichloroisocoumarin, Leupeptin, pepstatin, amastatin, ethylenediaminetetraacetic acid (EDTA) and 1,10 phenanthroline.
30 Protease assays performed over a pH range revealed that indeed protease(s) were present which exhibited maximal activity at ~ pH 8.0 (Table 16). Addition of DTT did not have any effect on protease activity. Crude broth was then treated with a variety of protease inhibitors (Table 17). Treatment of crude
35 broth with the inhibitors described above revealed that 1,10 phenanthroline caused complete inhibition of all protease activity when added at a final concentration of 50 μ g, with the IC_{50} = 5 μ g in 100 μ l of a 2 mg/ml crude broth solution. These data indicate that the most abundant protease(s) found in the

Table 17
Effect of different protease inhibitors on the protease activity
at pH 8 found in a Day 1 production of *Photobacterium luminescens*
(strain W-14).

5	Inhibitor	Corrected Flu. Units ^a	Percent Inhibition ^b
	Control	13053	0
	E-64	14259	0
10	1,10 Phenanthroline ^c	15	99
	3,4 Dichloroisocoumarin ^d	7956	39
	Leupeptin	13074	0
	Pepstatin ^c	13441	0
	Amastatin	12474	4
15	DMSO Control	12005	8
	Methanol Control	12125	7

a. Corrected Flu. Units = Fluorescence Units - background(2200 flu. units).

b. Percent Inhibition relative to protease activity at pH 8.0.

c. Inhibitors were dissolved in methanol.

d. Inhibitors were dissolved in DMSO.

The isolation of a zinc-metalloprotease was performed by applying dialyzed 10-80% ammonium sulfate pellet to a Q Sepharose column equilibrated at 50 mM Na₂PO₄, pH 7.0 as described in Example 5 for *Photobacterium* toxin. After extensive washing, a 0 to 0.5 M NaCl gradient was used to elute toxin protein. The majority of biological activity and protein was eluted from 0.15 - 0.45 M NaCl. However, it was observed that the majority of proteolytic activity was present in the 0.25-0.35 M NaCl fraction with some activity in the 0.15-0.25 M NaCl fraction. SDS PAGE analysis of the 0.25-0.35 M NaCl fraction showed a major peptide band of approximately 60 kDa. The 0.15-0.25 M NaCl fraction contained a similar 60 kDa band but at lower relative protein concentration. Subsequent gel filtration of this fraction using a Superose 12 HR 16/50 column resulted in a major peak migrating at 57.5 kDa that contained a predominant (> 90% of total stained protein) 58.5 kDa band by SDS PAGE analysis. Additional analysis of this fraction using various protease inhibitors as described above determined that the protease was a zinc-metalloprotease. Nearly all of the protease activity present in *Photobacterium* broth at day 1 of fermentation corresponded to the ~58 kDa zinc-metalloprotease.

In yet a second isolation of zinc-metalloprotease(s), W-14 *Photobacterium* broth grown for three days was taken and protease

activity was visualized using sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) laced with gelatin as described in Schmidt, T.M., Bleakley, B. and Nealson, K.M. 1988. SDS running gels (5.5 x 8 cm) were made with 12.5 %
5 polyacrylamide (40% stock solution of acrylamide/bis-acrylamide; Sigma Chemical Co., St. Louis, MO) into which 0.1% gelatin final concentration (Biorad EIA grade reagent; Richmond CA) was incorporated upon dissolving in water. SDS-stacking gels (1.0 x 8 cm) were made with 5% polyacrylamide, also laced with 0.1%
10 gelatin. Typically, 2.5 µg of protein to be tested was diluted in 0.03 ml of SDS-PAGE loading buffer without dithiothreitol (DTT) and loaded onto the gel. Proteins were electrophoresed in SDS running buffer (Laemmli, U.K. 1970. Nature 227, 680) at 0° C and at 8 mA. After electrophoresis was complete, the gel was
15 washed for 2 h in 2.5% (v/v) Triton X-100. Gels were then incubated for 1 h at 37 °C in 0.1 M glycine (pH 8.0). After incubation, gels were fixed and stained overnight with 0.1% amido black in methanol-acetic acid- water (30:10:60, vol./vol./vol.; Sigma Chemical Co.). Protease activity was visualized as light
20 areas against a dark, amido black stained background due to proteolysis and subsequent diffusion of incorporated gelatin. At least three distinct bands produced by proteolytic activity at 58-, 41-, and 38 kDa were observed.

Activity assays of the different proteases in W-14 day three
25 culture broth were performed using FITC-casein dissolved in water as substrate (0.02% final assay concentration). Proteolysis experiments were performed at 37 °C for 0-0.5 h in 0.1M Tris-HCl (pH 8.0) with different protein fractions in a total volume of 0.15 ml. Reactions were terminated by addition of an equal
30 volume of 12% trichloroacetic acid (TCA) dissolved in water. After incubation at room temperature for 0.25 h, samples were centrifuged at 10,000 x g for 0.25 h and 0.10 ml aliquots were removed and placed into 96-well microtiter plates. The solution was then neutralized by the addition of an equal volume of 2 N
35 sodium hydroxide, followed by quantitation using a Fluoroskan II fluorometric plate reader with excitation and emission wavelengths of 485 and 538 nm, respectively. Activity measurements were performed using FITC-Casein with different protease concentrations at 37° C for 0-10 min. A unit of

activity was arbitrarily defined as the amount of enzyme needed to produce 1000 fluorescent units/min and specific activity was defined as units/mg of protease.

Inhibition studies were performed using two zinc-metalloprotease inhibitors; 1,10 phenanthroline and N-(α -rhamnopyranosyloxyhydroxyphosphinyl)-Leu-Trp(phosphoramidon) with stock solutions of the inhibitors dissolved in 100% ethanol and water, respectively. Stock concentrations were typically 10 mg/ml and 5 mg/ml for 1,10 phenanthroline and phosphoramidon, respectively, with final concentrations of inhibitor at 0.5-1.0 mg/ml per reaction. Treatment of three day W-14 crude broth with 1,10 phenanthroline, an inhibitor of all zinc metalloproteases, resulted in complete elimination of all protease activity while treatment with phosphoramidon, an inhibitor of thermolysin-like proteases (Weaver, L.H., Kester, W.R., and Matthews, B.W. 1977. J. Mol. Biol. 114, 119-132), resulted in ~56% reduction of protease activity. The residual proteolytic activity could not be further reduced with additional phosphoramidon.

The proteases of three day W-14 *Photorhabdus* broth were purified as follows: 4.0 liters of broth were concentrated using an Amicon spiral ultra filtration cartridge Type SLY100 attached to an Amicon M-12 filtration device. The flow-through material having native proteins less than 100 kDa in size (3.8 L) was concentrated to 0.375 L using an Amicon spiral ultra filtration cartridge Type SLY10 attached to an Amicon M-12 filtration device. The retentate material contained proteins ranging in size from 10-100 kDa. This material was loaded onto a Pharmacia HR16/10 column which had been packed with PerSeptive Biosystem (Framington, MA) Poros® 50 HQ strong anion exchange packing that had been equilibrated in 10 mM sodium phosphate buffer (pH 7.0). Proteins were loaded on the column at a flow rate of 5 ml/min, followed by washing unbound protein with buffer until A₂₈₀ = 0.00. Afterwards, proteins were eluted using a NaCl gradient of 0-1.0 M NaCl in 40 min at a flow rate of 7.5 ml/min. Fractions were assayed for protease activity, *supra.*, and active fractions were pooled. Proteolytically active fractions were diluted with 50% (v/v) 10 mM sodium phosphate buffer (pH 7.0) and loaded onto a Pharmacia HR 10/10 Mono Q column equilibrated in 10 mM sodium phosphate. After washing the column with buffer until A₂₈₀ =

0.00, proteins were eluted using a NaCl gradient of 0-0.5 M NaCl for 1 h at a flow rate of 2.0 ml/min. Fractions were assayed for protease activity. Those fractions having the greatest amount of phosphoramidon-sensitive protease activity, the phosphoramidon sensitive activity being due to the 41/38 kDa protease, *infra.*, were pooled. These fractions were found to elute at a range of 0.15-0.25 M NaCl. Fractions containing a predominance of phosphoramidon-insensitive protease activity, the 58 kDa protease, were also pooled. These fractions were found to elute at a range of 0.25-0.35 M NaCl. The phosphoramidon-sensitive protease fractions were then concentrated to a final volume of 0.75 ml using a Millipore Ultrafree®-15 centrifugal filter device Biomax-5K NMWL membrane. This material was applied at a flow rate of 0.5 ml/min to a Pharmacia HR 10/30 column that had been packed with Pharmacia Sephadex G-50 equilibrated in 10 mM sodium phosphate buffer (pH 7.0)/ 0.1 M NaCl. Fractions having the maximal phosphoramidon-sensitive protease activity were then pooled and centrifuged over a Millipore Ultrafree®-15 centrifugal filter device Biomax-50K NMWL membrane. Proteolytic activity analysis, *supra.*, indicated this material to have only phosphoramidon-sensitive protease activity. Pooling of the phosphoramidon-insensitive protease, the 58 kDa protein, was followed by concentrating in a Millipore Ultrafree®-15 centrifugal filter device Biomax-50K NMWL membrane and further separation on a Pharmacia Superdex-75 column. Fractions containing the protease were pooled.

Analysis of purified 58- and 41/38 kDa purified proteases revealed that, while both types of protease were completely inhibited with 1,10 phenanthroline, only the 41/38 kDa protease was inhibited with phosphoramidon. Further analysis of crude broth indicated that protease activity of day 1 W-14 broth has 23% of the total protease activity due to the 41/38 kDa protease, increasing to 44% in day three W-14 broth.

Standard SDS-PAGE analysis for examining protein purity and obtaining amino terminal sequence was performed using 4-20% gradient MiniPlus SeptraGels purchased from Integrated Separation Systems (Natick, MA). Proteins to be amino-terminal sequenced were blotted onto PVDF membrane following purification, *infra.*, (ProBlott™ Membranes; Applied Biosystems, Foster City, CA).

visualized with 0.1% amido black, excised, and sent to Cambridge Prochem; Cambridge, MA, for sequencing.

Deduced amino terminal sequence of the 58- (SEQ ID NO:45) and 41/38 kDa (SEQ ID NO:44) proteases from three day old W-14 broth were DV-GSEKANEKLLK (SEQ ID NO: 45) and DSGDDDKVTNTDIHR (SEQ ID NO:44), respectively.

Sequencing of the 41/38 kDa protease revealed several amino termini, each one having an additional amino acid removed by proteolysis. Examination of the primary, secondary, tertiary and quaternary sequences for the 38 and 41 kDa polypeptides allowed for deduction of the sequence shown above and revealed that these two proteases are homologous.

Example 11, Part A

15 Screening of *Photorhabdus* Genomic Library via use of Antibodies for Genes encoding TcbA Peptide

In parallel to the sequencing described above, suitable probing and sequencing was done based on the TcbA_{ii} peptide (SEQ ID NO:1). This sequencing was performed by preparing bacterial culture broths and purifying the toxin as described in Examples 1 and 2 above.

Genomic DNA was isolated from the *Photorhabdus luminescens* strain W-14 grown in Grace's insect tissue culture medium. The bacteria were grown in 5 ml of culture medium in a 250 ml Erlenmeyer flask at 28°C and 250 rpm for approximately 24 hours. Bacterial cells from 100 ml of culture medium were pelleted at 5000 x g for 10 minutes. The supernatant was discarded, and the cell pellets then were used for the genomic DNA isolation.

30 The genomic DNA was isolated using a modification of the CTAB method described in Section 2.4.3 of Ausubel (*supra.*). The section entitled "Large Scale CsCl prep of bacterial genomic DNA" was followed through step 6. At this point, an additional chloroform/isoamyl alcohol (24:1) extraction was performed followed by a phenol/chloroform/isoamyl (25:24:1) extraction step and a final chloroform/isoamyl/alcohol (24:1) extraction. The DNA was precipitated by the addition of a 0.6 volume of isopropanol. The precipitated DNA was hooked and wound around the end of a bent glass rod, dipped briefly into 70% ethanol as a final wash, and dissolved in 3 ml of TE buffer.

FC 170370/10000

The DNA concentration, estimated by optical density at 280/260 nm, was approximately 2 mg/ml.

Using this genomic DNA, a library was prepared.

Approximately 50 µg of genomic DNA was partly digested with Sau3
5 Al. Then NaCl density gradient centrifugation was used to size
fractionate the partially digested DNA fragments. Fractions
containing DNA fragments with an average size of 12 kb, or
larger, as determined by agarose gel electrophoresis, were
ligated into the plasmid BluScript, Stratagene, La Jolla,
10 California, and transformed into an *E. coli* DH5α or DHB10 strain.

Separately, purified aliquots of the protein were sent to
the biotechnology hybridoma center at the University of
Wisconsin, Madison for production of monoclonal antibodies to the
proteins. The material that was sent was the HPLC purified
15 fraction containing native bands 1 and 2 which had been denatured
at 65°C, and 20 µg of which was injected into each of four mice.
Stable monoclonal antibody-producing hybridoma cell lines were
recovered after spleen cells from unimmunized mouse were fused
with a stable myeloma cell line. Monoclonal antibodies were
20 recovered from the hybridomas.

Separately, polyclonal antibodies were created by taking
native agarose gel purified band 1 (see Example 1) protein which
was then used to immunize a New Zealand white rabbit. The
protein was prepared by excising the band from the native agarose
25 gels, briefly heating the gel pieces to 65°C to melt the agarose,
and immediately emulsifying with adjuvant. Freund's complete
adjuvant was used for the primary immunizations and Freund's
incomplete was used for 3 additional injections at monthly
intervals. For each injection, approximately 0.2 ml of
30 emulsified band 1, containing 50 to 100 micrograms of protein,
was delivered by multiple subcutaneous injections into the back
of the rabbit. Serum was obtained 10 days after the final
injection and additional bleeds were performed at weekly
intervals for 3 weeks. The serum complement was inactivated by
35 heating to 56°C for 15 minutes and then stored at -20°C.

The monoclonal and polyclonal antibodies were then used to
screen the genomic library for the expression of antigens which
could be detected by the epitope. Positive clones were detected
on nitrocellulose filter colony lifts. An immunoblot analysis of
40 the positive clones was undertaken.

An analysis of the clones as defined by both immunoblot and Southern analysis resulted in the tentative identification of five classes of clones.

In the first class of clone was a gene encoding the peptide designated here as TcbA_{ii}. Full DNA sequence of this gene (TcbA) was obtained. It is set forth as SEQ ID NO:11. Confirmation that the sequence encodes the internal sequence of SEQ ID NO:1 is demonstrated by the presence of SEQ ID NO:1 at amino acid number 88 from the deduced amino acid sequence created by the open reading frame of SEQ ID NO:11. This can be confirmed by referring to SEQ ID NO:12, which is the deduced amino acid sequence created by SEQ ID NO:11.

The second class of toxin peptides contains the segments referred to above as TcaB_i, TcaB_{ii} and TcaC. Following the screening of the library with the polyclonal antisera, this second class of toxin genes was identified by several clones which produced different size proteins, all of which cross-reacted with the polyclonal antibody on an immunoblot and were also found to share DNA homology on a Southern Blot. Sequence comparison revealed that they belonged to the gene complex designated TcaB and TcaC above.

Three other classes of antibody toxin clones were also isolated in the polyclonal screen. These classes produced proteins that cross-react with a polyclonal antibody and also shared DNA homology with the classes as determined by Southern blotting. The classes have been designated Class III, Class IV and Class V. It was also possible to identify monoclonals that cross-reacted with Class I, II, III, and IV. This suggests that all have regions of high protein homology. Thus, it appears that the *P. luminescens* extracellular protein genes represent a family of genes which are evolutionarily related.

To further pursue the concept that there might be evolutionarily related variations in the toxin peptides contained within this organism, two approaches have been undertaken to examine other strains of *P. luminescens* for the presence of related proteins. This was done both by PCR amplification of genomic DNA and by immunoblot analysis using the polyclonal and monoclonal antibodies.

The results indicate that related proteins are produced by *P. luminescens* strains WX-2, WX-3, WX-4, WX-5, WX-6, WX-7, WX-8, WX-11, WX-12, WX-15 and W-14.

5

Example 11, Part BSequence and analysis of Class III toxin clones - tcc

Further DNA sequencing was performed on plasmids isolated from Class III *E. coli* clones described in Example 11, Part A. The nucleotide sequence was shown to be three closely linked open reading frames at this genomic locus. This locus was designated tcc with the three open reading frames designated tccA SEQ ID NO:56, tccB SEQ ID NO:58 and tccC SEQ ID NO:60 (Fig. 6B).

The deduced amino acid from the tccA open reading frame indicates the gene encodes a protein of 105,459 Da. This protein was designated TccA. The first 12 amino acids of this protein match the N-terminal sequence obtained from a 108 kDa protein, SEQ ID NO:7, previously identified as part of the toxin complex.

The deduced amino acid from the tccB open reading frame indicates this gene encodes a protein of 175,716 Da. This protein was designated TccB. The first 11 amino acids of this protein match the N-terminal sequence obtained from a protein with estimated molecular weight of 185 kDa, SEQ ID NO:8.

The deduced amino acid sequence of tccC indicated that this open reading frame encodes a protein of 111,694 Da and the protein product was designated TccC.

Example 12Characterization of *Photorhabdus* Strains

30

In order to establish that the collection described herein was comprised of *Photorhabdus* strains, the strains herein were assessed in terms of recognized microbiological traits that are characteristic of *Photorhabdus* and which differentiate it from other *Enterobacteriaceae* and *Xenorhabdus* spp. (Farmer, J.J. 1984. Bergey's Manual of Systemic Bacteriology, vol 1. pp. 510-511. (ed. Kreig N.R. and Holt, J.G.). Williams & Wilkins, Baltimore.; Akhurst and Boemare, 1988, Boemare et al., 1993). These characteristic traits are as follows: Gram's stain negative

rods, organism size of 0.5-2 μm in width and 2-10 μm in length, red/yellow colony pigmentation, presence of crystalline inclusion bodies, presence of catalase, inability to reduce nitrate, presence of bioluminescence, ability to take up dye from growth media, positive for protease production, growth-temperature range below 37°C, survival under anaerobic conditions and positively motile. (Table 18). Reference *Escherichia coli*, *Xenorhabdus* and *Photorhabdus* strains were included in all tests for comparison. The overall results are consistent with all strains being part of the family *Enterobacteriaceae* and the genus *Photorhabdus*.

A luminometer was used to establish the bioluminescence of each strain and provide a quantitative and relative measurement of light production. For measurement of relative light emitting units, the broths from each strain (cells and media) were measured at three time intervals after inoculation in liquid culture (6, 12, and 24 hr) and compared to background luminosity (uninoculated media and water). Prior to measuring light emission from the various broths, cell density was established by measuring light absorbance (560 nm) in a Gilford Systems (Oberlin, OH) spectrophotometer using a sipper cell. Appropriate dilutions were then made (to normalize optical density to 1.0 unit) before measuring luminosity. Aliquots of the diluted broths were then placed into cuvettes (300 μl each) and read in a Bio-Orbit 1251 Luminometer (Bio-Orbit Oy, Twiku, Finland). The integration period for each sample was 45 seconds. The samples were continuously mixed (spun in baffled cuvettes) while being read to provide oxygen availability. A positive test was determined as being ≥ 5 -fold background luminescence (~ 5 -10 units). In addition, colony luminosity was detected with photographic film overlays and visually, after adaptation in a darkroom. The Gram's staining characteristics of each strain were established with a commercial Gram's stain kit (BBL, Cockeysville, MD) used in conjunction with Gram's stain control slides (Fisher Scientific, Pittsburgh, PA). Microscopic evaluation was then performed using a Zeiss microscope (Carl Zeiss, Germany) 100X oil immersion objective lens (with 10X ocular and 2X body magnification). Microscopic examination of individual strains for organism size, cellular description and inclusion bodies (the latter after logarithmic growth) was

performed using wet mount slides (10X ocular, 2X body and 40X objective magnification) with oil immersion and phase contrast microscopy with a micrometer (Akhurst, R.J. and Boemare, N.E. 1990. Entomopathogenic Nematodes in Biological Control (ed. Gaugler, R. and Kaya, H.). pp. 75-90. CRC Press, Boca Raton, USA.; Baghdiguian S., Boyer-Giglio M.H., Thaler, J.O., Bonnot G., Boemare H. 1993. Biol. Cell 79, 177-185.). Colony pigmentation was observed after inoculation on Bacto nutrient agar, (Difco Laboratories, Detroit, MI) prepared as per label instructions.

10 Incubation occurred at 28°C and descriptions were produced after 5-7 days. To test for the presence of the enzyme catalase, a colony of the test organism was removed on a small plug from a nutrient agar plate and placed into the bottom of a glass test tube. One ml of a household hydrogen peroxide solution was gently

15 added down the side of the tube. A positive reaction was recorded when bubbles of gas (presumptive oxygen) appeared immediately or within 5 seconds. Controls of uninoculated nutrient agar and hydrogen peroxide solution were also examined. To test for nitrate reduction, each culture was inoculated into

20 10 ml of Bacto Nitrate Broth (Difco Laboratories, Detroit, MI). After 24 hours incubation at 28°C, nitrite production was tested by the addition of two drops of sulfanilic acid reagent and two drops of alpha-naphthylamine reagent (see Difco Manual, 10th edition, Difco Laboratories, Detroit, MI, 1984). The generation

25 of a distinct pink or red color indicates the formation of nitrite from nitrate. The ability of each strain to uptake dye from growth media was tested with Bacto MacConkey agar containing the dye neutral red; Bacto Tergitol-7 agar containing the dye bromothymol blue and Bacto EMB Agar containing the dye eosin-Y

30 (agars from Difco Laboratories, Detroit, MI, all prepared according to label instructions). After inoculation on these media, dye uptake was recorded after incubation at 28°C for 5 days. Growth on these latter media is characteristic for members of the family *Enterobacteriaceae*. Motility of each strain was

35 tested using a solution of Bacto Motility Test Medium (Difco Laboratories, Detroit, MI) prepared as per label instructions. A butt-stab inoculation was performed with each strain and motility was judged macroscopically by a diffuse zone of growth spreading from the line of inoculum. In many cases, motility was also

observed microscopically from liquid culture under wet mount slides. Biochemical nutrient evaluation for each strain was performed using BBL Enterotube II (Benton, Dickinson, Germany). Product instructions were followed with the exception that incubation was carried out at 28°C for 5 days. Results were consistent with previously cited reports for *Photorhabdus*. The production of protease was tested by observing hydrolysis of gelatin using Bacto gelatin (Difco Laboratories, Detroit, MI) plates made as per label instructions. Cultures were inoculated and the plates were incubated at 28°C for 5 days. To assess growth at different temperatures, agar plates [2% proteose peptone #3 with two percent Bacto-Agar (Difco, Detroit, MI) in deionized water] were streaked from a common source of inoculum. Plates were sealed with Nesco® film and incubated at 20, 28 and 37°C for up to three weeks. Plates showing no growth at 37°C showed no cell viability after transfer to a 28°C incubator for one week. Oxygen requirements for *Photorhabdus* strains were tested in the following manner. A butt-stab inoculation into fluid thioglycolate broth medium (Difco, Detroit, MI) was made. The tubes were incubated at room temperature for one week and cultures were then examined for type and extent of growth. The indicator resazurin demonstrates the level of medium oxidation or the aerobiosis zone (Difco Manual, 10th edition, Difco Laboratories, Detroit, MI). Growth zone results obtained for the *Photorhabdus* strains tested were consistent with those of a facultative anaerobic microorganism.

Table 18

Taxonomic Traits of *Photorhabdus* Strains

Strain	Traits Assessed*																	
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	
W-14	<u>-</u>	+	+	<u>rd</u> <u>S</u>	+	-	+	+	+	<u>O</u>	+	+	+	+	+	+	-	
WX-1	-	+	+	<u>rd</u> <u>S</u>	+	-	+	+	+	<u>O</u>	+	+	+	+	+	+	-	
WX-2	-	+	+	<u>rd</u> <u>S</u>	+	-	+	+	+	<u>O</u>	+	+	+	+	+	+	-	
WX-3	-	+	+	<u>rd</u> <u>S</u>	+	-	+	+	+	<u>YT</u>	+	+	+	+	+	+	-	
WX-4	-	+	+	<u>rd</u> <u>S</u>	+	-	+	+	+	<u>YT</u>	+	+	+	+	+	+	-	
WX-5	-	+	+	<u>rd</u> <u>S</u>	+	-	+	+	+	<u>LO</u>	+	+	+	+	+	+	-	

WX-6	-	+	+	rd S	+	-	+	+	+	LY	+	+	+	+	+	+	-
WX-7	-	+	+	rd S	+	-	+	+	+	R	+	+	+	+	+	+	-
WX-8	-	+	+	rd S	+	-	+	+	+	O	+	+	+	+	+	+	-
WX-9	-	+	+	rd S	+	-	+	+	+	YT	+	+	+	+	+	+	-
WX-10	-	+	+	rd S	+	-	+	+	+	Ro	+	+	+	+	+	+	-
WX-11	-	+	+	rd S	+	-	+	+	+	Ro	+	+	+	+	+	+	-
WX-12	-	+	+	rd S	+	-	+	+	+	O	+	+	+	+	+	+	-
WX-14	-	+	+	rd S	+	-	+	+	+	LR	+	+	+	+	+	+	-
WX-15	-	+	+	rd S	+	-	+	+	+	LR	+	+	+	+	+	+	-
H9	-	+	+	rd S	+	-	+	+	+	LY	+	+	+	+	+	+	-
Hb	-	+	+	rd S	+	-	+	+	+	YT	+	+	+	+	+	+	-
Hm	-	+	+	rd S	+	-	+	+	+	TY	+	+	+	+	+	+	-
HP88	-	+	+	rd S	+	-	+	+	+	LY	+	+	+	+	+	+	-
NC-1	-	+	+	rd S	+	-	+	+	+	O	+	+	+	+	+	+	-
W30	-	+	+	rd S	+	-	+	+	+	YT	+	+	+	+	+	+	-
WIR	-	+	+	rd S	+	-	+	+	+	RO	+	+	+	+	+	+	-
B2	-	+	+	rd S	+	-	+	+	+	R	+	+	+	+	+	+	-
43948	-	+	+	rd S	+	-	+	+	+	O	+	+	+	+	+	+	-
43949	-	+	+	rd S	+	-	+	+	+	O	+	+	+	+	+	+	-
43950	-	+	+	rd S	+	-	+	+	+	O	+	+	+	+	+	+	-
43951	-	+	+	rd S	+	-	+	+	+	O	+	+	+	+	+	+	-
43952	-	+	+	rd S	+	-	+	+	+	O	+	+	+	+	+	+	-

* - A = Gram's stain, B=Crystalline inclusion bodies,
 C=Bioluminescence, D=Cell form, E=Motility, F=Nitrate reduction,
 G=Presence of catalase, H=Gelatin hydrolysis, I=Dye uptake,
 J=Pigmentation, K=Growth on EMB agar, L=Growth on MacConkey agar,
 M=Growth on Tergitol-7 agar, N=Facultative anaerobe, O=Growth at
 20°C, P=Growth at 28°C, Q=Growth at 37°C, + - +/- = positive or
 negative for trait, rd=rod, S=sized within Genus descriptors,
 RO=red-orange, LR = light red, R= red, O= orange, Y= yellow, T=
 tan, LY= light yellow, YT= yellow tan, and LO= light orange.

Cellular fatty acid analysis is a recognized tool for
 bacterial characterization at the genus and species level
 (Tornabene, T.G. 1985. Lipid Analysis and the Relationship to

Chemotaxonomy in Methods in Microbiology, Vol 18, 202-214.;
Goodfellow, M. and O'Donnell, A.G. 1993. Roots of Bacterial
Systematics in Handbook of New Bacterial Systematics (ed.
Goodfellow, M. & O'Donnell, A.G.) pp. 3-54. London: Academic
5 Press Ltd.), these references are incorporated herein by
reference, and were used to confirm that our collection was
related at the genus level. Cultures were shipped to an
external, contract laboratory for fatty acid methyl ester
analysis (FAME) using a Microbial ID (MIDI, Newark, DE, USA)
10 Microbial Identification System (MIS). The MIS system consists of
a Hewlett Packard HP5890A gas chromatograph with a 25mm x 0.2mm
5% methylphenyl silicone fused silica capillary column. Hydrogen
is used as the carrier gas and a flame-ionization detector
functions in conjunction with an automatic sampler, integrator
15 and computer. The computer compares the sample fatty acid methyl
esters to a microbial fatty acid library and against a
calibration mix of known fatty acids. As selected by the
contract laboratory, strains were grown for 24 hours at 28°C on
trypticase soy agar prior to analysis. Extraction of samples was
20 performed by the contract lab as per standard FAME methodology.
There was no direct identification of the strains to any
luminescent bacterial group other than *Photorhabdus*. When the
cluster analysis was performed, which compares the fatty acid
profiles of a group of isolates, the strain fatty acid profiles
25 were related at the genus level.

The evolutionary diversity of the *Photorhabdus* strains in
our collection was measured by analysis of PCR (Polymerase Chain
Reaction) mediated genomic fingerprinting using genomic DNA from
each strain. This technique is based on families of repetitive
30 DNA sequences present throughout the genome of diverse bacterial
species (reviewed by Versalovic, J., Schneider, M., DE Bruijn,
F.J. and Lupski, J.R. 1994. *Methods Mol. Cell. Biol.*, 5, 25-40.).
Three of these, repetitive extragenic palindromic sequence (REP),
enterobacterial repetitive intergenic consensus (ERIC) and the
35 BOX element are thought to play an important role in the
organization of the bacterial genome. Genomic organization is
believed to be shaped by selection and the differential
dispersion of these elements within the genome of closely related
bacterial strains can be used to discriminate these strains (e.g.

Louws, F.J., Fulbright, D.W., Stephens, C.T. and DE Bruijn, F.J. 1994. Appl. Environ. Micro. 60, 2286-2295.). Rep-PCR utilizes oligonucleotide primers complementary to these repetitive sequences to amplify the variably sized DNA fragments lying
5 between them. The resulting products are separated by electrophoresis to establish the DNA "fingerprint" for each strain.

To isolate genomic DNA from our strains, cell pellets were resuspended in TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0) to a
10 final volume of 10 ml and 12 ml of 5 M NaCl was then added. This mixture was centrifuged 20 min. at 15,000 x g. The resulting pellet was resuspended in 5.7 ml of TE and 300 µl of 10% SDS and 60 µl 20 mg/ml proteinase K (Gibco BRL Products, Grand Island, NY) were added. This mixture was incubated at 37 °C for 1 hr.
15 approximately 10 mg of lysozyme was then added and the mixture was incubated for an additional 45 min. One milliliter of 5M NaCl and 800 µl of CTAB/NaCl solution (10% w/v CTAB, 0.7 M NaCl) were then added and the mixture was incubated 10 min. at 65°C, gently agitated, then incubated and agitated for an additional 20 min.
20 to aid in clearing of the cellular material. An equal volume of chloroform/isoamyl alcohol solution (24:1, v/v) was added, mixed gently then centrifuged. Two extractions were then performed with an equal volume of phenol/chloroform/isoamyl alcohol (50:49:1). Genomic DNA was precipitated with 0.6 volume of isopropanol.
25 Precipitated DNA was removed with a glass rod, washed twice with 70% ethanol, dried and dissolved in 2 ml of STE (10 mM Tris-HCl pH8.0, 10 mM NaCl, 1 mM EDTA). The DNA was then quantitated by optical density at 260 nm. To perform rep-PCR analysis of *Photorhabdus* genomic DNA the following primers were used, REP1R-
30 I; 5'-IIIICGICGICATCIGGC-3' and REP2-I; 5'-ICGICTTATCIGGCCTAC-3'. PCR was performed using the following 25µl reaction: 7.75 µl H₂O, 2.5 µl 10X LA buffer (PanVera Corp., Madison, WI), 16 µl dNTP mix (2.5 mM each), 1 µl of each primer at 50 pM/µl, 1 µl DMSO, 1.5 µl genomic DNA (concentrations ranged from 0.075-0.480 µg/µl) and
35 0.25 µl TaKaRa EX Taq (PanVera Corp., Madison, WI). The PCR amplification was performed in a Perkin Elmer DNA Thermal Cycler (Norwalk, CT) using the following conditions: 95°C/7 min. then 35 cycles of; 94°C/1 min., 44°C/1 min., 65°C/8 min., followed by 15 min. at 65°C. After cycling, the 25 µl reaction was added to 5 µl

of 5X gel loading buffer (0.25% bromophenol blue, 40% w/v sucrose in H₂O). A 15x20cm 1%-agarose gel was then run in TBE buffer (0.09 M Tris-borate, 0.002 M EDTA) using 8 ul of each reaction. The gel was run for approximately 16 hours at 45v. Gels were then
5 stained in 20 µg/ml ethidium bromide for 1 hour and destained in TBE buffer for approximately 3 hours. Polaroid® photographs of the gels were then taken under UV illumination.

The presence or absence of bands at specific sizes for each strain was scored from the photographs and entered as a
10 similarity matrix in the numerical taxonomy software program, NTSYS-pc (Exeter Software, Setauket, NY). Controls of *E. coli* strain HB101 and *Xanthomonas oryzae* pv. *oryzae* assayed at the same time produced PCR "fingerprints" corresponding to published reports (Versalovic, J., Koeuth, T. and Lupski, J.R. 1991.
15 Nucleic Acids Res. 19, 6823-6831; Vera Cruz, C.M., Halda-Alija, L., Louws, F., Skinner, D.Z., George, M.L., Nelson, R.J., DE Bruijn, F.J., Rice, C. and Leach, J.E. 1995. Int. Rice Res. Notes, 20, 23-24.; Vera Cruz, C.M., Ardales, E.Y., Skinner, D.Z., Talag, J., Nelson, R.J., Louws, F.J., Leung, H., Mew, T.W. and
20 Leach, J.E. 1996. Phytopathology (in press, respectively). The data from *Photorhabdus* strains were then analyzed with a series of programs within NTSYS-pc; SIMQUAL (Similarity for Qualitative data) to generate a matrix of similarity coefficients (using the Jaccard coefficient) and SAHN (Sequential, Agglomerative,
25 Heirarchical and Nested) clustering [using the UPGMA (Unweighted Pair-Group Method with Arithmetic Averages) method] which groups related strains and can be expressed as a phenogram (Figure 5). The COPH (cophenetic values) and MXCOMP (matrix comparison) programs were used to generate a cophenetic value matrix and
30 compare the correlation between this and the original matrix upon which the clustering was based. A resulting normalized Mantel statistic (r) was generated which is a measure of the goodness of fit for a cluster analysis (r=0.8-0.9 represents a very good fit). In our case r = 0.919. Therefore, our collection is
35 comprised of a diverse group of easily distinguishable strains representative of the *Photorhabdus* genus.

Example 13
Insecticidal Utility of Toxin(s) Produced
by Various *Photorhabdus* Strains

5 Initial "seed" cultures of the various *Photorhabdus* strains were produced by inoculating 175 ml of 2% Proteose Peptone #3 (PP3) (Difco Laboratories, Detroit, MI) liquid media with a primary variant subclone in a 500 ml tribaffled flask with a Delong neck, covered with a Kaput. Inoculum for each seed culture
10 was derived from oil-overlay agar slant cultures or plate cultures. After inoculation, these flasks were incubated for 16 hrs at 28°C on a rotary shaker at 150 rpm. These seed cultures were then used as uniform inoculum sources for a given fermentation of each strain. Additionally, overlaying the post-
15 log seed culture with sterile mineral oil, adding a sterile magnetic stir bar for future resuspension and storing the culture in the dark, at room temperature provided long-term preservation of inoculum in a toxin-competent state. The production broths were inoculated by adding 1% of the actively growing seed culture
20 to fresh 2% PP3 media (e.g. 1.75 ml per 175 ml fresh media). Production of broths occurred in either 500 ml tribaffled flasks (see above), or 2800 ml baffled, convex bottom flasks (500 ml volume) covered by a silicon foam closure. Production flasks were incubated for 24-48 hrs under the above mentioned
25 conditions. Following incubation, the broths were dispensed into sterile 1 L polyethylene bottles, spun at 2600 x g for 1 hr at 10°C and decanted from the cell and debris pellet. The liquid broth was then vacuum filtered through Whatman GF/D (2.7 µM retention) and GF/B (1.0 µM retention) glass filters to remove
30 debris. Further broth clarification was achieved with a tangential flow microfiltration device (Pall Filtron, Northborough, MA) using a 0.5 µM open-channel filter. When necessary, additional clarification could be obtained by chilling the broth (to 4°C) and centrifuging for several hours at 2600 x
35 g. Following these procedures, the broth was filter sterilized using a 0.2 µM nitrocellulose membrane filter. Sterile broths were then used directly for biological assay, biochemical analysis or concentrated (up to 15-fold) using a 10,000 MW cut-off, M12 ultra-filtration device (Amicon, Beverly MA) or

centrifugal concentrators (Millipore, Bedford, MA and Pall
Filtron, Northborough, MA) with a 10,000 MW pore size. In the
case of centrifugal concentrators, the broth was spun at 2000 x g
for approximately 2 hr. The 10,000 MW permeate was added to the
5 corresponding retentate to achieve the desired concentration of
components greater than 10,000 MW. Heat inactivation of
processed broth samples was achieved by heating the samples at
100°C in a sand-filled heat block for 10 minutes.

The broth(s) and toxin complex(es) from different
10 *Photorhabdus* strains are useful for reducing populations of
insects and were used in a method of inhibiting an insect
population which comprises applying to a locus of the insect an
effective insect inactivating amount of the active described. A
demonstration of the breadth of insecticidal activity observed
15 from broths of a selected group of *Photorhabdus* strains fermented
as described above is shown in Table 19. It is possible that
additional insecticidal activities could be detected with these
strains through increased concentration of the broth or by
employing different fermentation methods. Consistent with the
20 activity being associated with a protein, the insecticidal
activity of all strains tested was heat labile (see above).

Culture broth(s) from diverse *Photorhabdus* strains show
differential insecticidal activity (mortality and/or growth
inhibition, reduced adult emergence) against a number of insects.
25 More specifically, the activity is seen against corn rootworm
larvae and boll weevil larvae which are members of the insect
order Coleoptera. Other members of the Coleoptera include
wireworms, pollen beetles, flea beetles, seed beetles and
Colorado potato beetle. Activity is also observed against aster
30 leafhopper and corn plant hopper, which are members of the order
Homoptera. Other members of the Homoptera include planthoppers,
pear psylla, apple sucker, scale insects, whiteflies, spittle
bugs as well as numerous host specific aphid species. The broths
and purified toxin complex(es) are also active against tobacco
35 budworm, tobacco hornworm and European corn borer which are
members of the order Lepidoptera. Other typical members of this
order are beet armyworm, cabbage looper, black cutworm, corn
earworm, codling moth, clothes moth, Indian mealmoth, leaf
rollers, cabbage worm, cotton bollworm, bagworm, Eastern tent

caterpillar, sod webworm and fall armyworm. Activity is also seen against fruitfly and mosquito larvae which are members of the order *Diptera*. Other members of the order *Diptera* are, pea midge, carrot fly, cabbage root fly, turnip root fly, onion fly, crane fly and house fly and various mosquito species. Activity with broth(s) and toxin complex(es) is also seen against two-spotted spider mite which is a member of the order *Acarina* which includes strawberry spider mites, broad mites, citrus red mite, European red mite, pear rust mite and tomato russet mite.

Activity against corn rootworm larvae was tested as follows. *Photorhabdus* culture broth(s) (0-15 fold concentrated, filter sterilized), 2% Proteose Peptone #3, purified toxin complex(es) [0.23 mg/ml] or 10 mM sodium phosphate buffer, pH 7.0 were applied directly to the surface (about 1.5 cm²) of artificial diet (Rose, R. I. and McCabe, J. M. (1973). *J. Econ. Entomol.* 66, (398-400) in 40 µl aliquots. Toxin complex was diluted in 10 mM sodium phosphate buffer, pH 7.0. The diet plates were allowed to air-dry in a sterile flow-hood and the wells were infested with single, neonate *Diabrotica undecimpunctata howardi* (Southern corn rootworm, SCR) hatched from surface sterilized eggs. The plates were sealed, placed in a humidified growth chamber and maintained at 27°C for the appropriate period (3-5 days). Mortality and larval weight determinations were then scored. Generally, 16 insects per treatment were used in all studies. Control mortality was generally less than 5%.

Activity against boll weevil (*Anthonomus grandis*) was tested as follows. Concentrated (1-10 fold) *Photorhabdus* broths, control medium (2% Proteose Peptone #3), purified toxin complex(es) [0.23 mg/ml] or 10 mM sodium phosphate buffer, pH 7.0 were applied in 60 µl aliquots to the surface of 0.35 g of artificial diet (Stoneville Yellow lepidopteran diet) and allowed to dry. A single, 12-24 hr boll weevil larva was placed on the diet, and the wells were sealed and held at 25°C, 50% RH for 5 days. Mortality and larval weights were then assessed. Control mortality ranged between 0-13%.

Activity against mosquito larvae was tested as follows. The assay was conducted in a 96-well microtiter plate. Each well contained 200 µl of aqueous solution (10-fold concentrated *Photorhabdus* culture broth(s), control medium (2% Proteose

Peptone #3), 10 mM sodium phosphate buffer, toxin complex(es) @
0.23 mg/ml or H₂O) and approximately 20, 1-day old larvae (*Aedes*
aegypti). There were 6 wells per treatment. The results were
read at 3-4 days after infestation. Control mortality was
5 between 0-20%.

Activity against fruitflies was tested as follows.
Purchased *Drosophila melanogaster* medium was prepared using 50%
dry medium and a 50% liquid of either water, control medium (2%
Proteose Peptone #3), 10-fold concentrated *Photobacterium* culture
10 broth(s), purified toxin complex(es) [0.23 mg/ml] or 10 mM sodium
phosphate buffer, pH 7.0. This was accomplished by placing 4.0
ml of dry medium in each of 3 rearing vials per treatment and
adding 4.0 ml of the appropriate liquid. Ten late instar
Drosophila melanogaster maggots were then added to each 25 ml
15 vial. The vials were held on a laboratory bench, at room
temperature, under fluorescent ceiling lights. Pupal or adult
counts were made after 15 days of exposure. Adult emergence as
compared to water and control medium (0-16% reduction).

Activity against aster leafhopper adults (*Macrosteles*
20 *severini*) and corn planthopper nymphs (*Peregrinus maidis*) was
tested with an ingestion assay designed to allow ingestion of the
active without other external contact. The reservoir for the
active/"food" solution is made by making 2 holes in the center of
the bottom portion of a 35X10 mm Petri dish. A 2 inch Parafilm
25 M[®] square is placed across the top of the dish and secured with
an "O" ring. A 1 oz. plastic cup is then infested with
approximately 7 hoppers and the reservoir is placed on top of the
cup, Parafilm down. The test solution is then added to the
reservoir through the holes. In tests using 10-fold concentrated
30 *Photobacterium* culture broth(s), the broth and control medium (2%
Proteose Peptone #3) were dialyzed against 10 mM sodium phosphate
buffer, pH 7.0 and sucrose (to 5%) was added to the resulting
solution to reduce control mortality. Purified toxin complex(es)
[0.23 mg/ml] or 10 mM sodium phosphate buffer, pH 7.0 was also
35 tested. Mortality is reported at day 3. The assay was held in
an incubator at 28°C, 70% RH with a 16/8 photoperiod. The assays
were graded for mortality at 72 hours. Control mortality was
less than 6%.

Activity against lepidopteran larvae was tested as follows. Concentrated (10-fold) *Photorhabdus* culture broth(s), control medium (2% Proteose Peptone #3), purified toxin complex(es) [0.23 mg/ml] or 10 mM sodium phosphate buffer, pH 7.0 were applied directly to the surface (~1.5 cm²) of standard artificial lepidopteran diet (Stoneville Yellow diet) in 40 ul aliquots. The diet plates were allowed to air-dry in a sterile flow-hood and each well was infested with a single, neonate larva. European corn borer (*Ostrinia nubilalis*) and tobacco hornworm (*Manduca sexta*) eggs were obtained from commercial sources and hatched in-house, whereas tobacco budworm (*Heliothis virescens*) larvae were supplied internally. Following infestation with larvae, the diet plates were sealed, placed in a humidified growth chamber and maintained in the dark at 27°C for the appropriate period. Mortality and weight determinations were scored at day 5. Generally, 16 insects per treatment were used in all studies. Control mortality generally ranged from 4-12.5% for control medium and was less than 10% for phosphate buffer.

Activity against two-spotted spider mite (*Tetranychus urticae*) was determined as follows. Young squash plants were trimmed to a single cotyledon and sprayed to run-off with 10-fold concentrated broth(s), control medium (2% Proteose Peptone #3), purified toxin complex(es) [0.23 mg/ml] or 10 mM sodium phosphate buffer, pH 7.0. After drying, the plants were infested with a mixed population of spider mites and held at lab temperature and humidity for 72 hr. Live mites were then counted to determine levels of control.

Table 19
Observed Insecticidal Spectrum of Broths From Different
Photorhabdus Strains

5	<i>Photorhabdus</i> Strain	Sensitive* Insect Species
	WX-1	3**, 4, 5, 6, 7, 8
	WX-2	2, 4
	WX-3	1, 4
	WX-4	1, 4
10	WX-5	4
	WX-6	4
	WX-7	3, 4, 5, 6, 7, 8
	WX-8	1, 2, 4
	WX-9	1, 2, 4
15	WX-10	4
	WX-11	1, 2, 4
	WX-12	2, 4, 5, 6, 7, 8
	WX-14	1, 2, 4
	WX-15	1, 2, 4
20	W30	3, 4, 5, 8
	NC-1	1, 2, 3, 4, 5, 6, 7, 8, 9
	WIR	2, 3, 5, 6, 7, 8
	HP88	1, 3, 4, 5, 7, 8
	Hb	3, 4, 5, 7, 8
25	Hm	1, 2, 3, 4, 5, 7, 8
	H9	1, 2, 3, 4, 5, 6, 7, 8
	W-14	1, 2, 3, 4, 5, 6, 7, 8, 10
	ATCC 43948	4
	ATCC 43949	4
30	ATCC 43950	4
	ATCC 43951	4
	ATCC 43952	4

* = $\geq 25\%$ mortality and/or growth inhibition vs. control

35 ** = 1; Tobacco budworm, 2; European corn borer, 3;
Tobacco hornworm, 4; Southern corn rootworm, 5;
Boll weevil, 6; Mosquito, 7; Fruit Fly, 8;
Aster Leafhopper, 9; Corn planthopper, 10;
Two-spotted spider mite.

Example 14Non W-14 Photorhabdus Strains:Purification, Characterization and Activity Spectrum5 Purification

The protocol, as follows, is similar to that developed for the purification of W-14 and was established based on purifying those fractions having the most activity against Southern corn root worm (SCR), as determined in bioassays (see Example 13).

10 Typically, 4-20 L of broth that had been filtered, as described in Example 13, were received and concentrated using an Amicon spiral ultra filtration cartridge Type SLY100 attached to an Amicon M-12 filtration device. The retentate contained native proteins consisting of molecular sizes greater than 100 kDa,

15 whereas the flow through material contained native proteins less than 100 kDa in size. The majority of the activity against SCR was contained in the 100 kDa retentate. The retentate was then continually diafiltered with 10 mM sodium phosphate (pH = 7.0) until the filtrate reached an $A_{280} < 0.100$. Unless otherwise

20 stated, all procedures from this point were performed in buffer as defined by 10 mM sodium phosphate (pH 7.0). The retentate was then concentrated to a final volume of approximately 0.20 L and filtered using a 0.45 μ m Nalgene™ Filterware sterile filtration unit. The filtered material was loaded at 7.5 ml/min onto a

25 Pharmacia HR16/10 column which had been packed with PerSeptive Biosystem Poros® 50 HQ strong anion exchange matrix equilibrated in buffer using a PerSeptive Biosystem Sprint® HPLC system. After loading, the column was washed with buffer until an $A_{280} < 0.100$ was achieved. Proteins were then eluted from the column at

30 2.5 ml/min using buffer with 0.4 M NaCl for 20 min for a total volume of 50 ml. The column was then washed using buffer with 1.0 M NaCl at the same flow rate for an additional 20 min (final volume = 50 ml). Proteins eluted with 0.4 M and 1.0 M NaCl were placed in separate dialysis bags (Spectra/Por® Membrane MWCO:

35 2,000) and allowed to dialyze overnight at 4° C in 12 L buffer. The majority of the activity against SCR was contained in the 0.4 M fraction. The 0.4 M fraction was further purified by application of 20 ml to a Pharmacia XK 26/100 column that had been prepacked with Sepharose CL4B (Pharmacia) using a flow rate

of 0.75 ml/min. Fractions were pooled based on A280 peak profile and concentrated to a final volume of 0.75 ml using a Millipore Ultrafree®-15 centrifugal filter device Biomax-50K NMWL membrane. Protein concentrations were determined using a Biorad Protein Assay Kit with bovine gamma globulin as a standard.

Characterization

The native molecular weight of the SCR toxin complex was determined using a Pharmacia HR 16/50 that had been prepacked with Sepharose CL4B in buffer. The column was then calibrated using proteins of known molecular size thereby allowing for calculation of the toxin approximate native molecular size. As shown in Table 20, the molecular size of the toxin complex ranged from 777 kDa with strain Hb to 1,900 kDa with strain WX-14. The yield of toxin complex also varied, from strain WX-12 producing 0.8 mg/L to strain Hb, which produced 7.0 mg/L.

Proteins found in the toxin complex were examined for individual polypeptide size using SDS-PAGE analysis. Typically, 20 mg protein of the toxin complex from each strain was loaded onto a 2-15% polyacrylamide gel (Integrated Separation Systems) and electrophoresed at 20 mA in Biorad SDS-PAGE buffer. After completion of electrophoresis, the gels were stained overnight in Biorad Coomassie blue R-250 (0.2% in methanol: acetic acid: water; 40:10:40 v/v/v). Subsequently, gels were destained in methanol:acetic acid: water; 40:10:40 (v/v/v). The gels were then rinsed with water for 15 min and scanned using a Molecular Dynamics Personal Laser Densitometer®. Lanes were quantitated and molecular sizes were calculated as compared to Biorad high molecular weight standards, which ranged from 200-45 kDa.

Sizes of the individual polypeptides comprising the SCR toxin complex from each strain are listed in Table 21. The sizes of the individual polypeptides ranged from 230 kDa with strain WX-1 to a size of 16 kDa, as seen with strain WX-7. Every strain, with the exception of strain Hb, had polypeptides comprising the toxin complex that were in the 160-230 kDa range, the 100-160 kDa range, and the 50-80 kDa range. These data indicate that the toxin complex may vary in peptide composition and components from strain to strain, however, in all cases the

toxin attributes appears to consist of a large, oligomeric protein complex.

5

Table 20
Characterization of a Toxin Complex From
Non W-14 *Photorhabdus* Strains

Strain	Approx. Native Molecular Wt. ^a	Yield Active Fraction (mg/L) ^b
H9	972,000	1.8
Hb	777,000	7.0
Hm	1,400,000	1.1
HP88	813,000	2.5
NC1	1,092,000	3.3
WIR	979,000	1.0
WX-1	973,000	0.8
WX-2	951,000	2.2
WX-7	1,000,000	1.5
WX-12	898,000	0.4
WX-14	1,900,000	1.9
W-14	860,000	7.5
a Native molecular weight determined using a Pharmacia HP 16/50 column packed with Sepharose CL4B		
b Amount of toxin complex recovered from culture broth.		

Activity Spectrum

10 As shown in Table 21, the toxin complexes purified from strains Hm and H9 were tested for activity against a variety of insects, with the toxin complex from strain W-14 for comparison. The assays were performed as described in Example 13. The toxin complex from all three strains exhibited activity against tobacco
15 bud worm, European corn borer, Southern corn root worm, and aster leafhopper. Furthermore, the toxin complex from strains Hm and W-14 also exhibited activity against two-spotted spider mite. In addition, the toxin complex from W-14 exhibited activity against mosquito larvae. These data indicate that the toxin complex,
20 while having similarities in activities between certain orders of insects, can also exhibit differential activities against other orders of insects.

Table 21

The Approximate Sizes (in kDa) of Peptides in a Purified
Toxin Complex From Non W-14 *Photobhabdus*

5

H9	Hb	Hm	HP 88	NC-1	WIR	WX-1	WX-2	WX-7	WX-12	WX-14	W-14
180	150	170	170	180	170	230	200	200	180	210	190
170	140	140	160	170	160	190	170	180	160	180	180
160	139	100	140	140	120	170	150	110	140	160	170
140	130	81	130	110	110	160	120	87	139	120	160
120	120	72	129	44	89	110	110	75	130	110	150
98	100	68	110	16	79	98	82	43	110	100	130
87	98	49	100		74	76	64	33	92	95	120
84	88	46	86		62	58	37	28	87	80	110
79	81	30	81		51	53	30	26	80	69	93
72	75	22	77		40	41		23	73	49	90
68	69	20	73		39	35		22	59	41	77
60	60	19	60		37	31		21	56	33	69
57	57		58		33	28		19	51		65
52	54		45		30	24		18	37		63
46	49		39		28	22		16	33		60
40	44		35		27				32		51
37	39				25				26		46
	37				23						40
	35										39
											29

Table 22

Observed Insecticidal Spectrum of a Purified Toxin Complex from
Photorhabdus Strains

5	<u><i>Photorhabdus</i></u> Strain	Sensitive* Insect Species
	Hm Toxin Complex	1**, 2, 3, 5, 6, 7, 8
	H9 Toxin Complex	1, 2, 3, 6, 7, 8
10	W-14 Toxin Complex	1, 2, 3, 4, 5, 6, 7, 8
	* = > 25% mortality or growth inhibition	
	* = > 25% mortality or growth inhibition	
15	** = 1; Tobacco bud worm, 2; European corn borer, 3; Southern corn root worm, 4; Mosquito, 5; Two-spotted spider mite, 6; Aster Leafhopper, 7; Fruit Fly, 8; Boll Weevil	

Example 15

Sub-Fractionation of *Photorhabdus* Protein Toxin Complex

20

The *Photorhabdus* protein toxin complex was isolated as described in Example 14. Next, about 10 mg toxin was applied to a MonoQ 5/5 column equilibrated with 20 mM Tris-HCl, pH 7.0 at a flow rate of 1ml/min. The column was washed with 20 mM Tris-HCl, pH 7.0 until the optical density at 280 nm returned to baseline absorbance. The proteins bound to the column were eluted with a linear gradient of 0 to 1.0 M NaCl in 20 mM Tris-HCl, pH 7.0 at 1 ml/min for 30 min. One ml fractions were collected and subjected to Southern corn rootworm (SCR) bioassay (see Example 13). Peaks of activity were determined by a series of dilutions of each fraction in SCR bioassays. Two activity peaks against SCR were observed and were named A (eluted at about 0.2-0.3 M NaCl) and B (eluted at 0.3-0.4 M NaCl). Activity peaks A and B were pooled separately and both peaks were further purified using a 3-step procedure described below.

35

Solid (NH₄)₂SO₄ was added to the above protein fraction to a final concentration of 1.7 M. Proteins were then applied to a phenyl-Superose 5/5 column equilibrated with 1.7 M (NH₄)₂SO₄ in 50 mM potassium phosphate buffer, pH 7 at 1 ml/min. Proteins bound to the column were eluted with a linear gradient of 1.7 M (NH₄)₂SO₄, 0% ethylene glycol, 50 mM potassium phosphate, pH 7.0 to 25% ethylene glycol, 25 mM potassium phosphate, pH 7.0 (no (NH₄)₂SO₄) at 0.5 ml/min. Fractions were dialyzed overnight

40

against 10 mM sodium phosphate buffer, pH 7.0. Activities in each fraction against SCR were determined by bioassay.

The fractions with the highest activity were pooled and applied to a MonoQ 5/5 column which was equilibrated with 20 mM Tris-HCl, pH 7.0 at 1 ml/min. The proteins bound to the column were eluted at 1 ml/min by a linear gradient of 0 to 1M NaCl in 20 mM Tris-HCl, pH 7.0.

For the final step of purification, the most active fractions above (determined by SCR bioassay) were pooled and subjected to a second phenyl-Superose 5/5/ column. Solid $(\text{NH}_4)_2\text{SO}_4$ was added to a final concentration of 1.7 M. The solution was then loaded onto the column equilibrated with 1.7 M $(\text{NH}_4)_2\text{SO}_4$ in 50 mM potassium phosphate buffer, pH 7 at 1ml/min. Proteins bound to the column were eluted with a linear gradient of 1.7 M $(\text{NH}_4)_2\text{SO}_4$, 50 mM potassium phosphate, pH 7.0 to 10 mM potassium phosphate, pH 7.0 at 0.5 ml/min. Fractions were dialyzed overnight against 10 mM sodium phosphate buffer, pH 7.0. Activities in each fraction against SCR were determined by bioassay.

The final purified protein by the above 3-step procedure from peak A was named toxin A and the final purified protein from peak B was named toxin B.

Characterization and Amino Acid Sequencing of Toxin A and Toxin B

In SDS-PAGE, both toxin A and toxin B contained two major (> 90% of total Commassie stained protein) peptides: 192 kDa (named A1 and B1, respectively) and 58 kDa (named A2 and B2, respectively). Both toxin A and toxin B revealed only one major band in native PAGE, indicating A1 and A2 were subunits of one protein complex, and B1 and B2 were subunits of one protein complex. Further, the native molecular weight of both toxin A and toxin B were determined to be 860 kDa by gel filtration chromatography. The relative molar concentrations of A1 to A2 was judged to be a 1 to 1 equivalence as determined by densitometric analysis of SDS-PAGE gels. Similarly, B1 and B2 peptides were present at the same molar concentration.

Toxin A and toxin B were electrophoresed in 10% SDS-PAGE and transblotted to PVDF membranes. Blots were sent for amino acid analysis and N-terminal amino acid sequencing at Harvard MicroChem and Cambridge ProChem, respectively. The N-terminal

amino sequence of B1 was determined to be identical to SEQ ID NO:1, the TcbA_{ii} region of the *tcbA* gene (SEQ ID NO:12, position 87 to 99). A unique N-terminal sequence was obtained for peptide B2 (SEQ ID NO:40). The N-terminal amino acid sequence of peptide
5 B2 was identical to the TcbA_{iii} region of the derived amino acid sequence for the *tcbA* gene (SEQ ID NO:12, position 1935 to 1945). Therefore, the B toxin contained predominantly two peptides, TcbA_{ii} and TcbA_{iii}, that were observed to be derived from the same gene product, TcbA.

10 The N-terminal sequence of A2 (SEQ ID NO:41) was unique in comparison to the TcbA_{iii} peptide and other peptides. The A2 peptide was denoted TcdA_{iii} (see Example 17). SEQ ID NO:6 was determined to be a mixture of amino acid sequences SEQ ID NO:40 and 41.

15 Peptides A1 and A2 were further subjected to internal amino acid sequencing. For internal amino acid sequencing, 10 µg of toxin A was electrophoresized in 10% SDS-PAGE and transblotted to PVDF membrane. After the blot was stained with amido black, peptides A1 and A2, denoted TcdA_{ii} and TcdA_{iii}, respectively,
20 were excised from the blot and sent to Harvard MicroChem and Cambridge ProChem. Peptides were subjected to trypsin digestion followed by HPLC chromatography to separate individual peptides. N-terminal amino acid analysis was performed on selected tryptic peptide fragments. Two internal amino acid sequences of peptide
25 A1 (TcdA_{ii}-PK71, SEQ ID NO:38 and TcdA_{ii}-PK44, SEQ ID NO:39) were found to have significant homologies with deduced amino acid sequences of the TcbA_{ii} region of the *tcbA* gene (SEQ ID NO:12). Similarly, the N-terminal sequence (SEQ ID NO:41) and two
internal sequences of peptides A2 (TcdA_{iii}-PK57, SEQ ID NO:42 and
30 TcdA_{iii}-PK20, SEQ ID NO:43) also showed significant homology with deduced amino acid sequences of TcbA_{iii} region of the *tcbA* gene (SEQ ID NO:12).

In summary of above results, the toxin complex has at least two active protein toxin complexes against SCR; toxin A and toxin
35 B. Toxin A and toxin B are similar in their native and subunits molecular weight, however, their peptide compositions are different. Toxin A contained peptides TcdA_{ii} and TcdA_{iii} as the major peptides and the toxin B contains TcbA_{ii} and TcbA_{iii} as the major peptides.

Example 16Cleavage and Activation of TcbA Peptide

5

In the toxin B complex, peptide TcbA_{ii} and TcbA_{iii} originate from the single gene product TcbA (Example 15). The processing of TcbA peptide to TcbA_{ii} and TcbA_{iii} is presumably by the action of *Photorhabdus* protease(s), and most likely, the metalloproteases described in Example 10. In some cases, it was noted that when *Photorhabdus* W-14 broth was processed, TcbA peptide was present in toxin B complex as a major component, in addition to peptides TcbA_{ii} and TcbA_{iii}. Identical procedures, described for the purification of toxin B complex (Example 15), were used to enrich peptide TcbA from toxin complex fraction of W-14 broth. The final purified material was analyzed in a 4-20% gradient SDS-PAGE and major peptides were quantified by densitometry. It was determined that TcbA, TcbA_{ii} and TcbA_{iii} comprised 58%, 36%, and 6%, respectively, of total protein. The identities of these peptides were confirmed by their respective molecular sizes in SDS-PAGE and Western blot analysis using monospecific antibodies. The native molecular weight of this fraction was determined to be 860 kDa.

The cleavage of TcbA was evaluated by treating the above purified material with purified 38 kDa and 58 kDa W-14 *Photorhabdus* metalloproteases (Example 10), and Trypsin as a control enzyme (Sigma, MO). The standard reaction consisted 17.5 µg the above purified fraction, 1.5 unit protease, and 0.1 M Tris buffer, pH 8.0 in a total volume of 100 µl. For the control reaction, protease was omitted. The reaction mixtures were incubated at 37 °C for 90 min. At the end of the reaction, 20 µl was taken and boiled with SDS-PAGE sample buffer immediately for electrophoresis analysis in a 4-20% gradient SDS-PAGE. It was determined from SDS-PAGE that in both 38 kDa and 58 kDa protease treatments, the amount of peptides TcbA_{ii} and TcbA_{iii} increased about 3-fold while the amount of TcbA peptide decreased proportionally (Table 23). The relative reduction and augmentation of selected peptides was confirmed by Western blot analyses. Furthermore, gel filtration of the cleaved material revealed that the native molecular size of the complex remained the same. Upon trypsin treatment, peptides TcbA and TcbA_{ii} were

nonspecifically digested into small peptides. This indicated that 38 kDa and 58 kDa *Photorhabdus* proteases can specifically process peptide TcbA into peptides TcbA_{ii} and TcbA_{iii}. Protease treated and untreated control of the remaining 80 ul reaction mixture were serial diluted with 10 mM sodium phosphate buffer, pH 7.0 and analyzed by SCR bioassay. By comparing activity in several dilution, it was determined that the 38 kDa protease treatment increased SCR insecticidal activity approximately 3 to 4 fold. The growth inhibition of remaining insects in the protease treatment was also more severe than control (Table 23).

Table 23

Conversion and activation of peptide TcbA into peptides TcbA_{ii} and TcbA_{iii} by protease treatment.

	Control	38 kDa protease treatment
S0 (% of total protein)	58	18
S1 (% of total protein)	36	64
S9 (% of total protein)	6	18
LD50 (µg protein)	2.1	0.52
SCR Weight (mg/insect)*	0.2	0.1

*: an indication of growth inhibition by measuring the average weight of live insect after 5 days on diet in the assay.

Example 17

Screening of the library for a gene encoding the TcdA_{ii} Peptide

The cloning and characterization of a gene encoding the TcdA_{ii} peptide, described as SEQ ID NO:17 (internal peptide TcdA_{ii}-PT111 N-terminal sequence) and SEQ ID NO:18 (internal peptide TcdA_{ii}-PT79 N-terminal sequence) was completed. Two pools of degenerate oligonucleotides, designed to encode the amino acid sequences of SEQ ID NO:17 (Table 24) and SEQ ID NO:18 (Table 25), and the reverse complements of those sequences, were synthesized as described in Example 8. The DNA sequence of the oligonucleotides is given below:

Table 24
Degenerate Oligonucleotide for SEQ ID NO:17

P2-PT111	1	2	3	4	5	6	7	8
Amino Acid	Ala	Phe	Asn	Ile	Asp	Asp	Val	Ser
Codons	5' GCN	TT(T/C)	AA(T/C)	AT(T/C/A)	GA(T/C)	GA(T/C)	GTN 3'	
P2.3.6.CB	5' GC(A/C/G/T)	TT(T/C)	AAT	ATT	GAT	GAT	GT 3'	
P2.3.5	5' GC(A/C/G/T)	TT(T/C)	AA(T/C)	AT(T/C/A)	GA(T/C)	GA(T/C)	GT 3'	
P2.3.5R	5' AC	(G/A)TC	(G/A)TC	(T/G/A)AT	(G/A)TT	(G/A)AA	(A/C/G/T)GC 3'	
P2.3.5RI	5' ACI	TCI	TCI	ATI	TTI	AAI	GC 3'	
P2.3R.CB	5' CAG	(A/G)CT	(A/C)AC	ATC	ATC	AAT	ATT	AAA 3'

Table 25
Degenerate Oligonucleotide for SEQ ID NO:18

P2-PT79	1	2	3	4	5	6	7	8	9	10	11	12	13
Amino Acid	Phe	Ile	Val	Tyr	Thr	Ser	Leu	Gly	Val	Asn	Pro	Asn	Asn
Codons*	5' TTY	ATH	GTN	TAY	ACN	6	6	GGN	GTN	AAV	CCN	AAV	AAV 3'
P2.79.2	5' TTY	ATY	GTK	TAT	ACY	TCI	YTR	GGY	GTK	AAT	CCR	AAT	AAT 3'
P2.79.3	5' TTT	ATT	GTK	TAT	ACY	AGY	YTR	GGY	GTK	AAT	CCR	AAT	AAT 3'
P2.79.R.1	5' ATT	ATT	YGG	ATT	MAC	RCC	YAR	RCT	RGT	ATA	MAC	AAT	AAA 3'
P2.79R.CB	5' ATT	ATT	YGG	ATT	MAC	ACC	CAG	RCT	GGT	ATA	MAC	AAT	AAA 3'

* According to IUPAC-IUB codes for nucleotides, Y = C or T, H = A, C or T,
N = A, C, G or T, K = G or T, R = A or G, and M = A or C

Polymerase Chain Reactions (PCR) were performed essentially as described in Example 8, using as forward primers P2.3.5.CB or P2.3.5, and as reverse primers P2.79.R.1 or P2.79R.CB, in all forward/reverse combinations, using *Photorhabdus* W-14 genomic DNA as template. In another set of reactions, primers P2.79.2 or P2.79.3 were used as forward primers, and P2.3.5R, P2.3.5FI, and P2.3R.CB were used as reverse primers in all forward/reverse combinations. Only in the reactions containing P2.3.6.CB as the forward primers combined with P2.79.R.1 or P2.79R.CB as the reverse primers was a non-artifactual amplified product seen, of estimated size (mobility on agarose gels) of 2500 base pairs. The order of the primers used to obtain this amplification product indicates that the peptide fragment TcdA_{ii}-PT111 lies amino-proximal to the peptide fragment TcdA_{ii}-PT79.

The 2500 bp PCR products were ligated to the plasmid vector pCR[™]II (Invitrogen, San Diego, CA) according to the supplier's instructions, and the DNA sequences across the ends of the insert fragments of two isolates (HS24 and HS27) were determined using the supplier's recommended primers and the sequencing methods described previously. The sequence of both isolates was the same. New primers were synthesized based on the determined sequence, and used to prime additional sequencing reactions to obtain a total of 2557 bases of the insert [SEQ ID NO:36]. Translation of the partial peptide encoded by SEQ ID No: 36 yields the 845 amino acid sequence disclosed as SEQ ID NO:37. Protein homology analysis of this portion of the TcdA_{ii} peptide fragment reveals substantial amino acid homology (68% similarity; 53% identity) to residues 542 to 1390 of protein TcbA [SEQ ID NO:12]. It is therefore apparent that the gene represented in part by SEQ ID NO:36 produces a protein of similar, but not identical, amino acid sequence as the TcbA protein, and which likely has similar, but not identical biological activity as the TcbA protein.

In yet another instance, a gene encoding the peptides TcdA_{ii}-PK44 and the TcdA_{iii} 58 kDa N-terminal peptide, described as SEQ ID NO:9 (internal peptide TcdA_{ii}-PK44 sequence), and SEQ ID NO:41 (TcdA_{iii} 58 kDa N-terminal peptide sequence) was isolated. Two pools of degenerate oligonucleotides, designed to encode the amino acid sequences described as SEQ ID NO:39 (Table 27) and SEQ

ID NO:41 (Table 26), and the reverse complements of those sequences, were synthesized as described in Example 3, and their DNA sequences.

Table 26
Degenerate Oligonucleotide for SEQ ID NO:41

Codon #	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Amino Acid	Leu	Arg	Ser	Ala	Asn	Thr	Leu	Thr	Asp	Leu	Phe	Leu	Pro	Gln
A2.1	5' YTR	CGY	AGY	GCI	ANT	ACY	YTR	ACY	GAT	YTR	TTT	YTR	OCR	CA 3'
A2.2				GCI	ANT	ACI	YTR	ACI	GAY	YTR	TTY	YTR	OCI	CA 3'
A2.3.R		5' TG	YGG	YAR	AAA	YAR	RTC	RCG	YAR	RCG	RCG	IGC	RCG	3'
A2.4.R				5' TG	IGG	CPG	AAA	CPG	RTC	IGT	CAG	IGT	ATT	IEC 3'

Table 27
Degenerate Oligonucleotide for SEQ ID NO:39

Amino Acid #	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)	(16)
Codon #	1	2	3	4	5	6	7	8	9
Amino Acid	Gly	Pro	Val	Glu	Ile	Asn	Thr	Ala	Ile
A1.44.1	5' GGY	CCR	GTK	GAA	ATT	AAT	ACC	GCI	AT 3'
A1.44.1R	5' ATI	GCG	GTA	TTA	ATT	TCM	ACY	GGR	CC 3'
A1.44.2	5' GGI	CCI	GTI	GAR	ATY	AAV	ACI	GCI	AT 3'
A1.44.2R	5' ATI	GCI	GTR	TTR	ATY	TCI	ACI	GCI	CC 3'

Polymerase Chain Reactions (PCR) were performed essentially as described in Example 8, using as forward primers A1.44.1 or A1.44.2, and reverse primers A2.3R or A2.4R, in all forward/reverse combinations, using *Photorhabdus* W-14 genomic DNA as template. In another set of reactions, primers A2.1 or A2.2 were used as forward primers, and A1.44.1R, and A1.44.2R were used as reverse primers in all forward/reverse combinations. Only in the reactions containing A1.44.1 or A1.44.2 as the forward primers combined with A2.3R as the reverse primer was a non-artifactual amplified product seen, of estimated size (mobility on agarose gels) of 1400 base pairs. The order of the primers used to obtain this amplification product indicates that the peptide fragment TcdA_{iii}-PK44 lies amino-proximal to the 58 kDa peptide fragment of TcdA_{iii}.

The 1400 bp PCR products were ligated to the plasmid vector pCR[™]II according to the supplier's instructions. The DNA sequences across the ends of the insert fragments of four isolates were determined using primers similar in sequence to the supplier's recommended primers and using sequencing methods described previously. The nucleic acid sequence of all isolates differed as expected in the regions corresponding to the degenerate primer sequences, but the amino acid sequences deduced from these data were the same as the actual amino acid sequences for the peptides determined previously, (SEQ ID NOS:41 and 39).

Screening of the W-14 genomic cosmid library as described in Example 8 with a radiolabeled probe comprised of the DNA prepared above (SEQ ID NO:36) identified five hybridizing cosmid isolates, namely 17D9, 20B10, 21D2, 27B10, and 26D1. These cosmids were distinct from those previously identified with probes corresponding to the genes described as SEQ ID NO:11 or SEQ ID NO:25. Restriction enzyme analysis and DNA blot hybridizations identified three EcoR I fragments, of approximate sizes 3.7, 3.7, and 1.1 kbp, that span the region comprising the DNA of SEQ ID NO:36. Screening of the W-14 genomic cosmid library using as probe the radiolabeled 1.4 kbp DNA fragment prepared in this example identified the same five cosmids (17D9, 20B10, 21D2, 27B10, and 26D1). DNA blot hybridization to EcoR I-digested cosmid DNAs also showed hybridization to the same subset

of EcoR I fragments as seen with the 2.5 kbp TcdA_{ii} gene probe, indicating that both fragments are encoded on the genomic DNA.

DNA sequence determination of the cloned EcoR I fragments revealed an uninterrupted reading frame of 7551 base pairs (SEQ ID NO:46), encoding a 282.9 kDa protein of 2516 amino acids (SEQ ID NO:47). Analysis of the amino acid sequence of this protein revealed all expected internal fragments of peptides TcdA_{ii} (SEQ ID NOS:17, 18, 37, 38 and 39) and the TcdA_{iii} peptide N-terminus (SEQ ID NO:41) and all TcdA_{iii} internal peptides (SEQ ID NOS:42 and 43). The peptides isolated and identified as TcdA_{ii} and TcdA_{iii} are each products of the open reading frame, denoted *tcdA*, disclosed as SEQ ID NO:46. Further, SEQ ID NO:47 shows, starting at position 89, the sequence disclosed as SEQ ID NO:13, which is the N-terminal sequence of a peptide of size approximately 201 kDa, indicating that the initial protein produced from SEQ ID No: 46 is processed in a manner similar to that previously disclosed for SEQ ID NO:12. In addition, the protein is further cleaved to generate a product of size 209.2 kDa, encoded by SEQ ID NO:48 and disclosed as SEQ ID NO:49 (TcdA_{ii} peptide), and a product of size 63.6 kDa, encoded by SEQ ID NO:50 and disclosed as SEQ ID NO:51 (TcdA_{iii} peptide). Thus, it is thought that the insecticidal activity identified as toxin A (Example 15) derived from the products of SEQ ID NO:46, as exemplified by the full-length protein of 282.9 kDa disclosed as SEQ ID NO:47, is processed to produce the peptides disclosed as SEQ ID NOS:49 and 51. It is thought that the insecticidal activity identified as toxin B (Example 15) derives from the products of SEQ ID NO:11, as exemplified by the 280.6 kDa protein disclosed as SEQ ID NO:12. This protein is proteolytically processed to yield the 207.6 kDa peptide disclosed as SEQ ID NO:53, which is encoded by SEQ ID NO:52, and the 62.9 kDa peptide having N-terminal sequence disclosed as SEQ ID NO:40, and further disclosed as SEQ ID NO:55, which is encoded by SEQ ID NO:54.

Amino acid sequence comparisons between the proteins disclosed as SEQ ID NO:12 and SEQ ID NO:47 reveal that they have 69% similarity and 54% identity. This high degree of evolutionary relationship is not uniform throughout the entire amino acid sequence of these peptides, but is higher towards the carboxy-terminal end of the proteins, since the peptides

disclosed as SEQ ID NO:51 (derived from SEQ ID NO:47) and SEQ ID NO:55 (derived from SEQ ID NO:12) have 76% similarity and 64% identity.

5

Example 18

Control of European Cornborer-Induced Leaf Damage on Maize Plants
by Spray Application of *Photorhabdus* (Strain W-14) Broth

10 The ability of *Photorhabdus* toxin(s) to reduce plant damage
caused by insect larvae was demonstrated by measuring leaf damage
caused by European corn borer (*Ostrinia nubilalis*) infested onto
maize plants treated with *Photorhabdus* broth. Fermentation broth
from *Photorhabdus* strain W-14 was produced and concentrated
15 approximately 10-fold using ultrafiltration (10,000 MW pore-size)
as described in Example 13. The resulting concentrated broth was
then filter sterilized using 0.2 micron nitrocellulose membrane
filters. A similarly prepared sample of uninoculated 2% proteose
peptone #3 was used for control purposes. Maize plants (a
20 DowElanco proprietary inbred line) were grown from seed to
vegetative stage 7 or 8 in pots containing a soilless mixture in
a greenhouse (27°C day; 22°C night, about 50%RH, 14 hr day-
length, watered/fertilized as needed). The test plants were
arranged in a randomized complete block design (3 reps/treatment,
25 6 plants/treatment) in a greenhouse with temperature about 22°C
day; 18°C night, no artificial light and with partial shading,
about 50%RH and watered/fertilized as needed. Treatments
(uninoculated media and concentrated *Photorhabdus* broth) were
applied with a syringe sprayer, 2.0 mls applied from directly
30 (about 6 inches) over the whorl and 2.0 additional mls applied in
a circular motion from approximately one foot above the whorl.
In addition, one group of plants received no treatment. After
the treatments had dried (approximately 30 minutes), twelve
neonate European corn borer larvae (eggs obtained from commercial
35 sources and hatched in-house) were applied directly to the whorl.
After one week, the plants were scored for damage to the leaves
using a modified Guthrie Scale (Koziel, M. G., Beland, G. L.,
Bowman, C., Carozzi, N. B., Crenshaw, R., Crossland, L., Dawson,
J., Desai, N., Hill, M., Kadwell, S., Launis, K., Lewis, K.,
40 Maddox, D., McPherson, K., Meghji, M. Z., Merlin, E., Rhodes, R.,

Warren, G. W., Wright, M. and Evola, S. V. 1993).

Bio/Technology, 11, 194-195.) and the scores were compared statistically [T-test (LSD) $p < 0.05$ and Tukey's Studentized Range (HSD) Test $p < 0.1$]. The results are shown in Table 28. For reference, a score of 1 represents no damage, a score of 2 represents fine "window pane" damage on the unfurled leaf with no pinhole penetration and a score of 5 represents leaf penetration with elongated lesions and/or mid rib feeding evident on more than three leaves (lesions < 1 inch). These data indicate that broth or other protein containing fractions may confer protection against specific insect pests when delivered in a sprayable formulation or when the gene or derivative thereof, encoding the protein or part thereof, is delivered via a transgenic plant or microbe.

Table 28

Effect of *Photorhabdus* Culture Broth on
European Corn Borer-Induced Leaf Damage on Maize

20	Treatment	Average Guthrie Score
	No Treatment	5.02 ^a
	Uninoculated medium	5.15 ^a
	<i>Photorhabdus</i> Broth	2.24 ^b
25	(p<0.05 or p<0.1). Means with different letters are statistically different	

Example 19

Genetic Engineering of Genes for Expression in *E. coli*

30 Summary of constructions

A series of plasmids were constructed to express the *rcbA* gene of *Photorhabdus* W-14 in *Escherichia coli*. A list of the plasmids is shown in Table 29. A brief description of each construction follows as well as a summary of the *E. coli* expression data obtained.

Table 29
Expression plasmids for the *tcba* gene.

Plasmid	Gene	Vector/Selection	Compartment
pDAB634	<i>tcba</i>	pBC/Chl	Intracellular
pAcGP67B/ <i>tcba</i>	<i>tcba</i>	pAcGP67B/Amp	Baculovirus, secreted
pDAB635	<i>tcba</i>	pET27b/Kan	Periplasm
pET15- <i>tcba</i>	<i>tcba</i>	pET15- <i>tcba</i>	Intracellular

Abbreviations: Kan=kanamycin, Chl=chloramphenicol, Amp=ampicillin

5

Construction of pDAB634

In Example 9, a large EcoR I fragment which hybridizes to the *TcbA_{ii}* probe is described. This fragment was subcloned into pBC (Stratagene, La Jolla CA). Sequence analysis indicates that this fragment is 8816 base pairs. The fragment encodes the *tcba* gene with the initiating ATG at position 571 and the terminating TAA at position 8086. The fragment therefore carries 570 base pairs of *Photorhabdus* DNA upstream of the ATG and 730 base pairs downstream of the TAA.

15

Construction of Plasmid pAcGP67B/*tcba*

The *tcba* gene was PCR amplified using the following primers; 5' primer (SlAc51) 5' TTT AAA CCA TGG GAA ACT CAT TAT CAA GCA CTA TC 3' and 3' primer (SlAc31) 5' TTT AAA GCG GCC GCT TAA CGG ATG GTA TAA CGA ATA TG 3'. PCR was performed using a TaKaRa LA PCR kit from PanVera (Madison, Wisconsin) in the following reaction: 57.5 ml water, 10 ml 10X LA buffer, 16 ml dNTPs (2.5 mM each stock solution), 20 ml each primer at 10 pmoles/ml, 300 ng of the plasmid pDAB634 containing the W-14 *tcba* gene and one ml of TaKaRa LA Taq polymerase. The cycling conditions were 98°C/20 sec, 68°C/5 min, 72°C/10 min for 30 cycles. A PCR product of the expected about 7526bp was isolated in a 0.8% agarose gel in TBE (100 mM Tris, 90 mM boric acid, 1 mM EDTA) buffer and purified using a Qiaex II kit from Qiagen (Chatsworth, California). The purified *tcba* gene was digested with Nco I and Not I and ligated into the baculovirus transfer vector pAcGP67B (PharMingen (San Diego, California)) and transformed into DH5 α *E. coli*. The *tcba* gene was then cut from pAcGP67B and transferred to pET27b to create plasmid pDAB635. A missense mutation in the *tcba* gene was repaired in pDAB635.

The repaired *tcbA* gene contains two changes from the sequence shown in Sequence ID NO:11; an A>G at 212 changing an asparagine 71 to serine 71 and a G>A at 229 changing an alanine 77 to threonine 77. These changes are both upstream of the proposed TcbA_{ii} N-terminus.

Construction of pET15-*tcbA*

The *tcbA* coding region of pDAB635 was transferred to vector pET15b. This was accomplished using shotgun ligations, the DNAs were cut with restriction enzymes Nco I and Xho I. The resulting recombinant is called pET15-*tcbA*.

Expression of TcbA in *E. coli* from plasmid pET15-*tcbA*

Expression of *tcbA* in *E. coli* was obtained by modification of the methods previously described by Studier et al. (Studier, F.W., Rosenberg, A., Dunn, J., and Dubendorff, J., (1990) Use of T7 RNA polymerase to direct expression of cloned genes. Methods Enzymol., 185: 60-89.). Competent *E. coli* cells strain BL21(DE3) were transformed with plasmid pET15-*tcbA* and plated on LB agar containing 100 µg/ml ampicillin and 40 mM glucose. The transformed cells were plated to a density of several hundred isolated colonies/plate. Following overnight incubation at 37°C the cells were scraped from the plates and suspended in LB broth containing 100 µg /ml ampicillin. Typical culture volumes were from 200-500 ml. At time zero, culture densities (OD600) were from 0.05-0.15 depending on the experiment. Cultures were shaken at one of three temperatures (22°C, 30°C or 37°C) until a density of 0.15-0.5 was obtained at which time they were induced with 1 mM isopropylthio-β-galactoside (IPTG). Cultures were incubated at the designated temperature for 4-5 hours and then were transferred to 4°C until processing (12-72 hours).

Purification and characterization of TcbA expressed in *E.coli* from Plasmid pET15-*tcbA*.

E. coli cultures expressing TcbA peptides were processed as follows. Cells were harvested by centrifugation at 17,000 x G and the media was decanted and saved in a separate container.

The media was concentrated about 8x using the M12 (Amicon, Beverly MA) filtration system and a 100 kD molecular mass cut-off filter. The concentrated media was loaded onto an anion exchange

column and the bound proteins were eluted with 1.0 M NaCl. The 1.0 M NaCl elution peak was found to cause mortality against Southern corn rootworm (SCR) larvae (Table 30). The 1.0 M NaCl fraction was dialyzed against 10 mM sodium phosphate buffer pH 7.0, concentrated, and subjected to gel filtration on Sepharose CL-4B (Pharmacia, Piscataway, New Jersey). The region of the CL-4B elution profile corresponding to calculated molecular weight (about 900 kDa) as the native W-14 toxin complex was collected, concentrated and bioassayed against larvae. The collected 900 kDa fraction was found to have insecticidal activity (see Table 30 below), with symptomology similar to that caused by native W-14 toxin complex. This fraction was subjected to Proteinase K and heat treatment, the activity in both cases was either eliminated or reduced, providing evidence that the activity is proteinaceous in nature. In addition, the active fraction tested immunologically positive for the TcbA and TcbA_{iii} peptides in immunoblot analysis when tested with an anti-TcbA_{iii} monoclonal antibody (Table 30).

20

Table 30

Results of Immunoblot and SCR Bioassays.

Fraction	SCR Activity		Immunoblot Peptides Detected	Native Size [CL-4B Estimated Size]
	% Mortality	% Growth Inhibit.		
TcbA Media 1.0 M Ion Exchange	+++	+++	TcbA	
TcbA Media CL-4B	+++	+++	TcbA, TcbA _{iii}	~900 kDa
TcbA Media CL-4B + Proteinase K	++	+++	NT	
TcbA Media CL-4B + heat treatment	-	-	NT	
TcbA Cell Sup CL-4B	-	+++	NT	~900 kD

PK = Proteinase K treatment 2 hours; Heat treatment = 100°C for 10 minutes; ND = None Detected; NT = Not Tested. Scoring system for mortality and growth inhibition as compared to control samples; 5-24%="+", 25-49%="++", 50-100%="+++".

The cell pellet was resuspended in 10 mM sodium phosphate buffer, pH=7.0, and lysed by passage through a Bio-Neb™ cell nebulizer (Glas-Col Inc., Terra Haute, IN). The pellets were

5 treated with DNase to remove DNA and centrifuged at 17,000 x g to
separate the cell pellet from the cell supernatant. The
supernatant fraction was decanted and filtered through a 0.2
micron filter to remove large particles and subjected to anion
10 exchange chromatography. Bound proteins were eluted with 1.0 M
NaCl, dialyzed and concentrated using Biomax™ (Millipore Corp,
Bedford, MA) concentrators with a molecular mass cut-off of
50,000 Daltons. The concentrated fraction was subjected to gel
filtration chromatography using Sepharose CL-4B beaded matrix.
15 Bioassay data for material prepared in this way is shown in Table
30 and is denoted as "TcbA Cell Sup".

In yet another method to handle large amounts of material,
the cell pellets were re-suspended in 10 mM sodium phosphate
buffer, pH = 7.0 and thoroughly homogenized by using a Kontes
15 Glass Company (Vineland, NJ) 40 ml tissue grinder. The cellular
debris was pelleted by centrifugation at 25,000 x g and the cell
supernatant was decanted, passed through a 0.2 micron filter and
subjected to anion exchange chromatography using a Pharmacia
10/10 column packed with Poros HQ 50 beads. The bound proteins
20 were eluted by performing a NaCl gradient of 0.0 to 1.0 M.
Fractions containing the TcbA protein were combined and
concentrated using a 50 kDa concentrator and subjected to gel
filtration chromatography using Pharmacia CL-4B beaded matrix.
The fractions containing TcbA oligomer, molecular mass of
25 approximately 900 kDa, were collected and subjected to anion
exchange chromatography using a Pharmacia Mono Q 10/10 column
equilibrated with 20 mM Tris buffer pH = 7.3. A gradient of 0.0
to 1.0 M NaCl was used to elute recombinant TcbA protein.
Recombinant TcbA eluted from the column at a salt concentration
30 of approximately 0.3-0.4 M NaCl, the same molarity at which
native TcbA oligomer is eluted from the Mono Q 10/10 column. The
recombinant TcbA fraction was found to cause SCR mortality in
bioassay experiments similar to those in Table 30.

35

SEQUENCE LISTING

- 5 (1) GENERAL INFORMATION:
- 10 (i) APPLICANT: Ensign, Jerald C
Bowen, David J
Petell, James
Fatig, Raymond
Schoonover, Sue
French-Constant, Richard
Orr, Gregory L
Merlo, Donald J
15 Roberts, Jean L
Rocheleau, Thomas A
Blackburn, Michael B
Hey, Timothy D
Strickland, James A
- 20 (ii) TITLE OF INVENTION: Insecticidal Protein Toxins From
Photorhabdus
- (iii) NUMBER OF SEQUENCES: 61
- 25 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Quarles & Brady
(B) STREET: 1 South Pinckney Street
(C) CITY: Madison
(D) STATE: WI
30 (E) COUNTRY: US
(F) ZIP: 53703
- (v) COMPUTER READABLE FORM:
35 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent In Release #1.0, Version #1.30
- 40 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- 45 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/063,615
(B) FILING DATE: 18-MAY-1993
- 50 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/395,497
(B) FILING DATE: 28-FEB-1995
- 55 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/007,255
(B) FILING DATE: 06-NOV-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/608,423
(B) FILING DATE: 28-FEB-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/705,484

(B) FILING DATE: 23-AUG-1996

5

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seay, Nicholas J

(B) REGISTRATION NUMBER: 27386

(C) REFERENCE/DOCKET NUMBER: 960296.93804

10

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 608-251-5000

(B) TELEFAX: 608-251-9166

15

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Phe	Ile	Gln	Gly	Tyr	Ser	Asp	Leu	Phe	Gly	Asn
1				5					10	

35

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gln	Asp	Ser	Pro	Glu	Val	Ser	Ile	Thr	Thr	Trp
1				5					10		

55

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10 Ser Glu Ser Leu Phe Thr Gln Thr Leu Lys Glu Ala Arg Arg Asp Ala
1 5 10 15
Leu Val Ala

15 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30 Ala Ser Pro Leu Ser Thr Ser Glu Leu Thr Ser Lys Leu Asn
1 5 10

35 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

50 Ala Gly Asp Thr Ala Asn Ile Gly Asp
1 5

(2) INFORMATION FOR SEQ ID NO:6:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
60 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu Gly Gly Ala Ala Thr Leu Leu Asp Leu Leu Leu Pro Gln Ile
1 5 10 15

10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Leu Ser Thr Met Glu Lys Gln Leu Asn Glu
1 5 10

30 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

45 Met Asn Leu Ala Ser Pro Leu Ile Ser
1 5

50 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

60 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ile Asn Leu Asp Ile Asn Glu Gln Asn Lys Ile Met Val Val Ser
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Ala Lys Asp Val Lys Phe Gly Ser Asp Ala Arg Val Lys Met Leu
 1 5 10 15
 Arg Gly Val Asn
 20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7515 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..7515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG CAA AAC TCA TTA TCA AGC ACT ATC GAT ACT ATT TGT CAG AAA CTG 48
 Met Gln Asn Ser Leu Ser Ser Thr Ile Asp Thr Ile Cys Gln Lys Leu
 1 5 10 15
 CAA TTA ACT TGT CCG GCG GAA ATT GCT TTG TAT CCC TTT GAT ACT TTC 95
 Gln Leu Thr Cys Pro Ala Glu Ile Ala Leu Tyr Pro Phe Asp Thr Phe
 20 25 30
 CGG GAA AAA ACT CGG GGA ATG GTT AAT TGG GGG GAA GCA AAA CGG ATT 144
 Arg Glu Lys Thr Arg Gly Met Val Asn Trp Gly Glu Ala Lys Arg Ile
 35 40 45
 TAT GAA ATT GCA CAA GCG GAA CAG GAT AGA AAC CTA CTT CAT GAA AAA 192
 Tyr Glu Ile Ala Gln Ala Glu Gln Asp Arg Asn Leu Leu His Glu Lys
 50 55 60
 CGT ATT TTT GCC TAT GCT AAT CCG CTG CTG AAA AAC GCT GTT CGG TTG 240
 Arg Ile Phe Ala Tyr Ala Asn Pro Leu Leu Lys Asn Ala Val Arg Leu

	65	70	75	80	
5	GGT ACC CGG CAA ATG TTG GGT TTT ATA CAA GGT TAT AGT GAT CTG TTT Gly Thr Arg Gln Met Leu Gly Phe Ile Gln Gly Tyr Ser Asp Leu Phe	85	90	95	283
10	GGT AAT CGT GCT GAT AAC TAT GCC GCG CCG GGC TCG GTT GCA TCG ATG Gly Asn Arg Ala Asp Asn Tyr Ala Ala Pro Gly Ser Val Ala Ser Met	100	105	110	336
15	TTC TCA CCG GCG GCT TAT TTG ACG GAA TTG TAC CGT GAA GCC AAA AAC Phe Ser Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Lys Asn	115	120	125	384
20	TTG CAT GAC AGC AGC TCA ATT TAT TAC CTA GAT AAA CGT CCG CCG GAT Leu His Asp Ser Ser Ser Ile Tyr Tyr Leu Asp Lys Arg Arg Pro Asp	130	135	140	432
25	TTA GCA AGC TTA ATG CTC AGC CAG AAA AAT ATG GAT GAG GAA ATT TCA Leu Ala Ser Leu Met Leu Ser Gln Lys Asn Met Asp Glu Glu Ile Ser	145	150	155	480
30	ACG CTG GCT CTC TCT AAT GAA TTG TGC CTT GCC GGG ATC GAA ACA AAA Thr Leu Ala Leu Ser Asn Glu Leu Cys Leu Ala Gly Ile Glu Thr Lys	155	160	165	528
35	ACA GGA AAA TCA CAA GAT GAA GTG ATG GAT ATG TTG TCA ACT TAT CGT Thr Gly Lys Ser Gln Asp Glu Val Met Asp Met Leu Ser Thr Tyr Arg	170	175	180	576
40	TTA AGT GGA GAG ACA CCT TAT CAT CAC GCT TAT GAA ACT GTT CGT GAA Leu Ser Gly Glu Thr Pro Tyr His His Ala Tyr Glu Thr Val Arg Glu	180	185	190	624
45	ATC GTT CAT GAA CGT GAT CCA GGA TTT CGT CAT TTG TCA CAG GCA CCC Ile Val His Glu Arg Asp Pro Gly Phe Arg His Leu Ser Gln Ala Pro	195	200	205	672
50	ATT GTT GCT GCT AAG CTC GAT CCT GTG ACT TTG TTG GGT ATT AGC TCC Ile Val Ala Ala Lys Leu Asp Pro Val Thr Leu Leu Gly Ile Ser Ser	210	215	220	720
55	CAT ATT TCG CCA GAA CTG TAT AAC TTG CTG ATT GAG GAG ATC CCG GAA His Ile Ser Pro Glu Leu Tyr Asn Leu Leu Ile Glu Glu Ile Pro Glu	225	230	235	768
60	AAA GAT GAA GCC GCG CTT GAT ACG CTT TAT AAA ACA AAC TTT GGC GAT Lys Asp Glu Ala Ala Leu Asp Thr Leu Tyr Lys Thr Asn Phe Gly Asp	245	250	255	816
65	ATT ACT ACT GCT CAG TTA ATG TCC CCA AGT TAT CTG GCC CGG TAT TAT Ile Thr Thr Ala Gln Leu Met Ser Pro Ser Tyr Leu Ala Arg Tyr Tyr	260	265	270	864
70	GGC GTC TCA CCG GAA GAT ATT GCC TAC GTG ACG ACT TCA TTA TCA CAT Gly Val Ser Pro Glu Asp Ile Ala Tyr Val Thr Thr Ser Leu Ser His	275	280	285	912
75	GTT GGA TAT AGC AGT GAT ATT CTG GTT ATT CCG TTG GTC GAT GGT GTG Val Gly Tyr Ser Ser Asp Ile Leu Val Ile Pro Leu Val Asp Gly Val	290	295	300	960
80	GGT AAG ATG GAA GTA GTT CGT GTT ACC CGA ACA CCA TCG GAT AAT TAT Gly Lys Met Glu Val Val Arg Val Thr Arg Thr Pro Ser Asp Asn Tyr	305	310	315	1008
85		325	330	335	

ACC AGT CAG ACG AAT TAT ATT GAG CTG TAT CCA CAG GGT GGC GAC AAT 1056
 Thr Ser Gln Thr Asn Tyr Ile Glu Leu Tyr Pro Gln Gly Gly Asp Asn
 340 345 350

5 TAT TTG ATC AAA TAC AAT CTA AGC AAT AGT TTT GGT TTG GAT GAT TTT 1104
 Tyr Leu Ile Lys Tyr Asn Leu Ser Asn Ser Phe Gly Leu Asp Asp Phe
 355 360 365

10 TAT CTG CAA TAT AAA GAT GGT TCC GCT GAT TGG ACT GAG ATT GCC CAT 1152
 Tyr Leu Gln Tyr Lys Asp Gly Ser Ala Asp Trp Thr Glu Ile Ala His
 370 375 380

15 AAT CCC TAT CCT GAT ATG GTC ATA AAT CAA AAG TAT GAA TCA CAG GCG 1200
 Asn Pro Tyr Pro Asp Met Val Ile Asn Gln Lys Tyr Glu Ser Gln Ala
 385 390 395 400

20 ACA ATC AAA CGT AGT GAC TCT GAC AAT ATA CTC AGT ATA GGG TTA CAA 1248
 Thr Ile Lys Arg Ser Asp Ser Asp Asn Ile Leu Ser Ile Gly Leu Gln
 405 410 415

AGA TGG CAT AGC GGT AGT TAT AAT TTT GCC GCC GCC AAT TTT AAA ATT 1296
 Arg Trp His Ser Gly Ser Tyr Asn Phe Ala Ala Ala Asn Phe Lys Ile
 420 425 430

25 GAC CAA TAC TCC CCG AAA GCT TTC CTG CTT AAA ATG AAT AAG GCT ATT 1344
 Asp Gln Tyr Ser Pro Lys Ala Phe Leu Leu Lys Met Asn Lys Ala Ile
 435 440 445

30 CGG TTG CTC AAA GCT ACC GGC CTC TCT TTT GCT ACG TTG GAG CGT ATT 1392
 Arg Leu Leu Lys Ala Thr Gly Leu Ser Phe Ala Thr Leu Glu Arg Ile
 450 455 460

35 GTT GAT AGT GTT AAT AGC ACC AAA TCC ATC ACG GTT GAG GTA TTA AAC 1440
 Val Asp Ser Val Asn Ser Thr Lys Ser Ile Thr Val Glu Val Leu Asn
 465 470 475 480

AAG GTT TAT CGG GTA AAA TTC TAT ATT GAT CGT TAT GGC ATC AGT GAA 1488
 Lys Val Tyr Arg Val Lys Phe Tyr Ile Asp Arg Tyr Gly Ile Ser Glu
 485 490 495

40 GAG ACA GCC GCT ATT TTG GCT AAT ATT AAT ATC TCT CAG CAA GCT GTT 1536
 Glu Thr Ala Ala Ile Leu Ala Asn Ile Asn Ile Ser Gln Gln Ala Val
 500 505 510

45 GGC AAT CAG CTT AGC CAG TTT GAG CAA CTA TTT AAT CAC CCG CCG CTC 1584
 Gly Asn Gln Leu Ser Gln Phe Glu Gln Leu Phe Asn His Pro Pro Leu
 515 520 525

50 AAT GGT ATT CGC TAT GAA ATC AGT GAG GAC AAC TCC AAA CAT CTT CCT 1632
 Asn Gly Ile Arg Tyr Glu Ile Ser Glu Asp Asn Ser Lys His Leu Pro
 530 535 540

55 AAT CCT GAT CTG AAC CTT AAA CCA GAC AGT ACC GGT GAT GAT CAA CGC 1580
 Asn Pro Asp Leu Asn Leu Lys Pro Asp Ser Thr Gly Asp Asp Gln Arg
 545 550 555 560

AAG GCG GTT TTA AAA CGC GCG TTT CAG GTT AAC GCC AGT GAG TTG TAT 1728
 Lys Ala Val Leu Lys Arg Ala Phe Gln Val Asn Ala Ser Glu Leu Tyr
 565 570 575

60 CAG ATG TTA TTG ATC ACT GAT CGT AAA GAA GAC GGT GTT ATC AAA AAT 1776
 Gln Met Leu Leu Ile Thr Asp Arg Lys Glu Asp Gly Val Ile Lys Asn
 580 585 590

65 AAC TTA GAG AAT TTG TCT GAT CTG TAT TTG GTT AGT TTG CTG GCC CAG 1824
 Asn Leu Glu Asn Leu Ser Asp Leu Tyr Leu Val Ser Leu Leu Ala Gln

	595	600	605
5	ATT CAT AAC CTG ACT ATT GCT GAA TTG AAC ATT TTG TTG GTG ATT TGT 1872 Ile His Asn Leu Thr Ile Ala Glu Leu Asn Ile Leu Leu Val Ile Cys 610 615 620		
10	GGC TAT GGC GAC ACC AAC ATT TAT CAG ATT ACC GAC GAT AAT TTA GCC 1920 Gly Tyr Gly Asp Thr Asn Ile Tyr Gln Ile Thr Asp Asp Asn Leu Ala 625 630 635 640		
15	AAA ATA GTG GAA ACA TTG TTG TGG ATC ACT CAA TGG TTG AAG ACC CAA 1968 Lys Ile Val Glu Thr Leu Leu Trp Ile Thr Gln Trp Leu Lys Thr Gln 645 650 655		
20	AAA TGG ACA GTT ACC GAC CTG TTT CTG ATG ACC ACG GCC ACT TAC AGC 2016 Lys Trp Thr Val Thr Asp Leu Phe Leu Met Thr Thr Ala Thr Tyr Ser 660 665 670		
25	ACC ACT TTA ACG CCA GAA ATT AGC AAT CTG ACG GCT ACG TTG TCT TCA 2064 Thr Thr Leu Thr Pro Glu Ile Ser Asn Leu Thr Ala Thr Leu Ser Ser 675 680 685		
30	ACT TTG CAT GGC AAA GAG AGT CTG ATT GGG GAA GAT CTG AAA AGA GCA 2112 Thr Leu His Gly Lys Glu Ser Leu Ile Gly Glu Asp Leu Lys Arg Ala 690 695 700		
35	ATG GCG CCT TGC TTC ACT TCG GCT TTG CAT TTG ACT TCT CAA GAA GTT 2160 Met Ala Pro Cys Phe Thr Ser Ala Leu His Leu Thr Ser Gln Glu Val 705 710 715 720		
40	GCG TAT GAC CTG CTG TTG TGG ATA GAC CAG ATT CAA CCG GCA CAA ATA 2208 Ala Tyr Asp Leu Leu Leu Trp Ile Asp Gln Ile Gln Pro Ala Gln Ile 725 730 735		
45	ACT GTT GAT GGG TTT TGG GAA GAA GTG CAA ACA ACA CCA ACC AGC TTG 2256 Thr Val Asp Gly Phe Trp Glu Glu Val Gln Thr Thr Pro Thr Ser Leu 740 745 750		
50	AAG GTG ATT ACC TTT GCT CAG GTG CTG GCA CAA TTG AGC CTG ATC TAT 2304 Lys Val Ile Thr Phe Ala Gln Val Leu Ala Gln Leu Ser Leu Ile Tyr 755 760 765		
55	CGT CGT ATT GGG TTA AGT GAA ACG GAA CTG TCA CTG ATC GTG ACT CAA 2352 Arg Arg Ile Gly Leu Ser Glu Thr Glu Leu Ser Leu Ile Val Thr Gln 770 775 780		
60	TCT TCT CTG CTA GTG GCA GGC AAA AGC ATA CTG GAT CAC GGT CTG TTA 2400 Ser Ser Leu Leu Val Ala Gly Lys Ser Ile Leu Asp His Gly Leu Leu 785 790 795 800		
65	ACC CTG ATG GCC TTG GAA GGT TTT CAT ACC TGG GTT AAT GGC TTG GGG 2448 Thr Leu Met Ala Leu Glu Gly Phe His Thr Trp Val Asn Gly Leu Gly 805 810 815		
70	CAA CAT GCC TCC TTG ATA TTG GCG GCG TTG AAA GAC GGA GCC TTG ACA 2496 Gln His Ala Ser Leu Ile Leu Ala Ala Leu Lys Asp Gly Ala Leu Thr 820 825 830		
75	GTT ACC CAT GTA GCA CAA GCT ATG AAT AAG GAG GAA TCT CTC CTA CAA 2544 Val Thr Asp Val Ala Gln Ala Met Asn Lys Glu Glu Ser Leu Leu Gln 835 840 845		
80	ATG GCA GCT AAT CAG GTG GAG AAG GAT CTA ACA AAA CTG ACC AGT TGG 2592 Met Ala Ala Asn Gln Val Glu Lys Asp Leu Thr Lys Leu Thr Ser Trp 850 855 860		

	ACA CAG ATT GAC GCT ATT CTG CAA TGG TTA CAG ATG TCT TCG GCC TTG 2640	
	Thr Gln Ile Asp Ala Ile Leu Gln Trp Leu Gln Met Ser Ser Ala Leu	
	865 870 875 880	
5	GCG GTT TCT CCA CTG GAT CTG GCA GGG ATG ATG GCC CTG AAA TAT GGG 2688	
	Ala Val Ser Pro Leu Asp Leu Ala Gly Met Met Ala Leu Lys Tyr Gly	
	885 890 895	
10	ATA GAT CAT AAC TAT GCT GCC TGG CAA GCT GCG GCG GCT GCG CTG ATG 2736	
	Ile Asp His Asn Tyr Ala Ala Trp Gln Ala Ala Ala Ala Leu Met	
	900 905 910	
15	GCT GAT CAT GCT AAT CAG GCA CAG AAA AAA CTG GAT GAG ACG TTC AGT 2784	
	Ala Asp His Ala Asn Gln Ala Gln Lys Lys Leu Asp Glu Thr Phe Ser	
	915 920 925	
20	AAG GCA TTA TGT AAC TAT TAT ATT AAT GCT GTT CTC GAT AGT GCT GCT 2832	
	Lys Ala Leu Cys Asn Tyr Tyr Ile Asn Ala Val Val Asp Ser Ala Ala	
	930 935 940	
	GGA GTA CGT GAT CGT AAC GGT TTA TAT ACC TAT TTG CTG ATT GAT AAT 2880	
	Gly Val Arg Asp Arg Asn Gly Leu Tyr Thr Tyr Leu Leu Ile Asp Asn	
	945 950 955 960	
25	CAG GTT TCT GCC GAT GTG ATC ACT TCA CGT ATT GCA GAA GCT ATC GCC 2928	
	Gln Val Ser Ala Asp Val Ile Thr Ser Arg Ile Ala Glu Ala Ile Ala	
	965 970 975	
30	GGT ATT CAA CTG TAC GTT AAC CGG GCT TTA AAC CGA GAT GAA GGT CAG 2976	
	Gly Ile Gln Leu Tyr Val Asn Arg Ala Leu Asn Arg Asp Glu Gly Gln	
	980 985 990	
35	CTT GCA TCG GAC GTT AGT ACC CGT CAG TTC TTC ACT GAC TGG GAA CGT 3024	
	Leu Ala Ser Asp Val Ser Thr Arg Gln Phe Phe Thr Asp Trp Glu Arg	
	995 1000 1005	
40	TAC AAT AAA CGT TAC AGT ACT TGG GCT GGT GTC TCT GAA CTG GTC TAT 3072	
	Tyr Asn Lys Arg Tyr Ser Thr Trp Ala Gly Val Ser Glu Leu Val Tyr	
	1010 1015 1020	
	TAT CCA GAA AAC TAT GTT GAT CCC ACT CAG CGC ATT GGG CAA ACC AAA 3120	
	Tyr Pro Glu Asn Tyr Val Asp Pro Thr Gln Arg Ile Gly Gln Thr Lys	
	1025 1030 1035 1040	
45	ATG ATG GAT GCG CTG TTG CAA TCC ATC AAC CAG AGC CAG CTA AAT GCG 3168	
	Met Met Asp Ala Leu Leu Gln Ser Ile Asn Gln Ser Gln Leu Asn Ala	
	1045 1050 1055	
50	GAT ACG GTG GAA GAT GCT TTC AAA ACT TAT TTG ACC AGC TTT GAG CAG 3216	
	Asp Thr Val Glu Asp Ala Phe Lys Thr Tyr Leu Thr Ser Phe Glu Gln	
	1060 1065 1070	
55	GTA GCA AAT CTG AAA GTA ATT AGT GCT TAC CAC GAT AAT GTG AAT GTG 3264	
	Val Ala Asn Leu Lys Val Ile Ser Ala Tyr His Asp Asn Val Asn Val	
	1075 1080 1085	
60	GAT CAA GGA TTA ACT TAT TTT ATC GGT ATC GAC CAA GCA GCT CCG GGT 3312	
	Asp Gln Gly Leu Thr Tyr Phe Ile Gly Ile Asp Gln Ala Ala Pro Gly	
	1090 1095 1100	
	ACG TAT TAC TGG CGT AGT GTT GAT CAC AGC AAA TGT GAA AAT GGC AAG 3360	
	Thr Tyr Tyr Trp Arg Ser Val Asp His Ser Lys Cys Glu Asn Gly Lys	
	1105 1110 1115 1120	
65	TTT GCC GCT AAT GCT TGG GGT GAG TGG AAT AAA ATT ACC TGT GCT GTC 3408	
	Phe Ala Ala Asn Ala Trp Gly Glu Trp Asn Lys Ile Thr Cys Ala Val	

	1125	1130	1135
5	AAT CCT TGG AAA AAT ATC ATC CGT CCG GTT GTT TAT ATG TCC CGC TTA 3456 Asn Pro Trp Lys Asn Ile Ile Arg Pro Val Val Tyr Met Ser Arg Leu 1140 1145 1150		
10	TAT CTG CTA TGG CTG GAG CAG CAA TCA AAG AAA AGT GAT GAT GGT AAA 3504 Tyr Leu Leu Trp Leu Glu Gln Gln Ser Lys Lys Ser Asp Asp Gly Lys 1155 1160 1165		
15	ACC ACG ATT TAT CAA TAT AAC TTA AAA CTG GCT CAT ATT CGT TAC GAC 3552 Thr Thr Ile Tyr Gln Tyr Asn Leu Lys Leu Ala His Ile Arg Tyr Asp 1170 1175 1180		
20	GGT AGT TGG AAT ACA CCA TTT ACT TTT GAT GTG ACA GAA AAG GTA AAA 3600 Gly Ser Trp Asn Thr Pro Phe Thr Phe Asp Val Thr Glu Lys Val Lys 1185 1190 1195 1200		
25	AAT TAC ACG TCG AGT ACT GAT GCT GCT GAA TCT TTA GGG TTG TAT TGT 3648 Asn Tyr Thr Ser Ser Thr Asp Ala Ala Glu Ser Leu Gly Leu Tyr Cys 1205 1210 1215		
30	ACT GGT TAT CAA GGG GAA GAC ACT CTA TTA GTT ATG TTC TAT TCG ATG 3696 Thr Gly Tyr Gln Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Ser Met 1220 1225 1230		
35	CAG AGT AGT TAT AGC TCC TAT ACC GAT AAT AAT GCG CCG GTC ACT GGG 3744 Gln Ser Ser Tyr Ser Ser Tyr Thr Asp Asn Asn Ala Pro Val Thr Gly 1235 1240 1245		
40	CTA TAT ATT TTC GCT GAT ATG TCA TCA GAC AAT ATG ACG AAT GCA CAA 3792 Leu Tyr Ile Phe Ala Asp Met Ser Ser Asp Asn Met Thr Asn Ala Gln 1250 1255 1260		
45	GCA ACT AAC TAT TGG AAT AAC AGT TAT CCG CAA TTT GAT ACT GTG ATG 3840 Ala Thr Asn Tyr Trp Asn Asn Ser Tyr Pro Gln Phe Asp Thr Val Met 1265 1270 1275 1280		
50	GCA GAT CCG GAT AGC GAC AAT AAA AAA GTC ATA ACC AGA AGA GTT AAT 3888 Ala Asp Pro Asp Ser Asp Asn Lys Lys Val Ile Thr Arg Arg Val Asn 1285 1290 1295		
55	AAC CGT TAT GCG GAG GAT TAT GAA ATT CCT TCC TCT GTG ACA AGT AAC 3936 Asn Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Thr Ser Asn 1300 1305 1310		
60	AGT AAT TAT TCT TGG GGT GAT CAC AGT TTA ACC ATG CTT TAT GGT GGT 3984 Ser Asn Tyr Ser Trp Gly Asp His Ser Leu Thr Met Leu Tyr Gly Gly 1315 1320 1325		
65	AGT GTT CCT AAT ATT ACT TTT GAA TCG GCG GCA GAA GAT TTA AGG CTA 4032 Ser Val Pro Asn Ile Thr Phe Glu Ser Ala Ala Glu Asp Leu Arg Leu 1330 1335 1340		
	TCT ACC AAT ATG GCA TTG AGT ATT ATT CAT AAT GGA TAT GCG GGA ACC 4080 Ser Thr Asn Met Ala Leu Ser Ile Ile His Asn Gly Tyr Ala Gly Thr 1345 1350 1355 1360		
	CGC CGT ATA CAA TGT AAT CTT ATG AAA CAA TAC GCT TCA TTA GGT GAT 4128 Arg Arg Ile Gln Cys Asn Leu Met Lys Gln Tyr Ala Ser Leu Gly Asp 1365 1370 1375		
	AAA TTT ATA ATT TAT GAT TCA TCA TTT GAT GAT GCA AAC CGT TTT AAT 4176 Lys Phe Ile Ile Tyr Asp Ser Ser Phe Asp Asp Ala Asn Arg Phe Asn 1380 1385 1390		

CTG GTG CCA TTG TTT AAA TTC GGA AAA GAC GAG AAC TCA GAT GAT AGT 4321
 Leu Val Pro Leu Phe Lys Phe Gly Lys Asp Glu Asn Ser Asp Asp Ser
 1395 1400 1405

5 ATT TGT ATA TAT AAT GAA AAC CCT TCC TCT GAA GAT AAG AAG TGG TAT 427
 Ile Cys Ile Tyr Asn Glu Asn Pro Ser Ser Glu Asp Lys Lys Trp Tyr
 1410 1415 1420

10 TTT TCT TCG AAA GAT GAC AAT AAA ACA GCG GAT TAT AAT GGT GGA ACT 432
 Phe Ser Ser Lys Asp Asp Asn Lys Thr Ala Asp Tyr Asn Gly Gly Thr
 1425 1430 1435 1440

15 CAA TGT ATA GAT GCT GGA ACC AGT AAC AAA GAT TTT TAT TAT AAT CTC 436
 Gln Cys Ile Asp Ala Gly Thr Ser Asn Lys Asp Phe Tyr Tyr Asn Leu
 1445 1450 1455

20 CAG GAG ATT GAA GTA ATT AGT GTT ACT GGT GGG TAT TGG TCG AGT TAT 441
 Gln Glu Ile Glu Val Ile Ser Val Thr Gly Gly Tyr Trp Ser Ser Tyr
 1460 1465 1470

AAA ATA TCC AAC CCG ATT AAT ATC AAT ACG GGC ATT GAT AGT GCT AAA 4461
 Lys Ile Ser Asn Pro Ile Asn Ile Asn Thr Gly Ile Asp Ser Ala Lys
 1475 1480 1485

25 GTA AAA GTC ACC GTA AAA GCG GGT GGT GAC GAT CAA ATC TTT ACT GCT 451
 Val Lys Val Thr Val Lys Ala Gly Gly Asp Asp Gln Ile Phe Thr Ala
 1490 1495 1500

30 GAT AAT AGT ACC TAT GTT CCT CAG CAA CCG GCA CCC AGT TTT GAG GAG 456
 Asp Asn Ser Thr Tyr Val Pro Gln Gln Pro Ala Pro Ser Phe Glu Glu
 1505 1510 1515 1520

35 ATG ATT TAT CAG TTC AAT AAC CTG ACA ATA GAT TGT AAG AAT TTA AAT 460
 Met Ile Tyr Gln Phe Asn Asn Leu Thr Ile Asp Cys Lys Asn Leu Asn
 1525 1530 1535

40 TTC ATC GAC AAT CAG GCA CAT ATT GAG ATT GAT TTC ACC GCT ACG GCA 465
 Phe Ile Asp Asn Gln Ala His Ile Glu Ile Asp Phe Thr Ala Thr Ala
 1540 1545 1550

CAA GAT GGC CGA TTC TTG GGT GCA GAA ACT TTT ATT ATC CCG GTA ACT 4704
 Gln Asp Gly Arg Phe Leu Gly Ala Glu Thr Phe Ile Ile Pro Val Thr
 1555 1560 1565

45 AAA AAA GTT CTC GGT ACT GAG AAC GTG ATT CCG TTA TAT AGC GAA AAT 4752
 Lys Lys Val Leu Gly Thr Glu Asn Val Ile Ala Leu Tyr Ser Glu Asn
 1570 1575 1580

50 AAC GGT GTT CAA TAT ATG CAA ATT GGC GCA TAT CGT ACC CGT TTG AAT 4800
 Asn Gly Val Gln Tyr Met Gln Ile Gly Ala Tyr Arg Thr Arg Leu Asn
 1585 1590 1595 1600

55 ACG TTA TTC GCT CAA CAG TTG GTT AGC CGT GCT AAT CGT GGC ATT GAT 4848
 Thr Leu Phe Ala Gln Gln Leu Val Ser Arg Ala Asn Arg Gly Ile Asp
 1605 1610 1615

60 GCA GTG CTC AGT ATG GAA ACT CAG AAT ATT CAG GAA CCG CAA TTA CGA 4896
 Ala Val Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu Gly
 1620 1625 1630

CCG GGC ACA TAT GTG CAG CTT GTG TTG GAT AAA TAT GAT GAG TCT ATT 4944
 Ala Gly Thr Tyr Val Gln Leu Val Leu Asp Lys Tyr Asp Glu Ser Ile
 1635 1640 1645

65 CAT GGC ACT AAT AAA AGC TTT GCT ATT GAA TAT GTT GAT ATA TTT AAA 4992
 His Gly Thr Asn Lys Ser Phe Ala Ile Glu Tyr Val Asp Ile Phe Lys

	1650	1655	1660	
5	GAG AAC GAT AGT TTT GTG ATT TAT CAA GGA GAA CTT AGC GAA ACA AGT 5040 Glu Asn Asp Ser Phe Val Ile Tyr Gln Gly Glu Leu Ser Glu Thr Ser 1665 1670 1675 1680			
10	CAA ACT GTT GTG AAA GTT TTC TTA TCC TAT TTT ATA GAG GCG ACT GGA 5088 Gln Thr Val Val Lys Val Phe Leu Ser Tyr Phe Ile Glu Ala Thr Gly 1685 1690 1695			
15	AAT AAG AAC CAC TTA TGG GTA CGT GCT AAA TAC CAA AAG GAA ACG ACT 5136 Asn Lys Asn His Leu Trp Val Arg Ala Lys Tyr Gln Lys Glu Thr Thr 1700 1705 1710			
20	GAT AAG ATC TTG TTC GAC CGT ACT GAT GAG AAA GAT CCG CAC GGT TGG 5184 Asp Lys Ile Leu Phe Asp Arg Thr Asp Glu Lys Asp Pro His Gly Trp 1715 1720 1725			
25	TTT CTC AGC GAC GAT CAC AAG ACC TTT AGT GGT CTC TCT TCC GCA CAG 5232 Phe Leu Ser Asp Asp His Lys Thr Phe Ser Gly Leu Ser Ser Ala Gln 1730 1735 1740			
30	GCA TTA AAG AAC GAC AGT GAA CCG ATG GAT TTC TCT GGC GCC AAT GCT 5280 Ala Leu Lys Asn Asp Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ala 1745 1750 1755 1760			
35	CTC TAT TTC TGG GAA CTG TTC TAT TAC ACG CCG ATG ATG ATG GCT CAT 5328 Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro Met Met Met Ala His 1765 1770 1775			
40	CGT TTG TTG CAG GAA CAG AAT TTT GAT GCG GCG AAC CAT TGG TTC CGT 5376 Arg Leu Leu Gln Glu Gln Asn Phe Asp Ala Ala Asn His Trp Phe Arg 1780 1785 1790			
45	TAT GTC TGG AGT CCA TCC GGT TAT ATC GTT GAT GGT AAA ATT GCT ATC 5424 Tyr Val Trp Ser Pro Ser Gly Tyr Ile Val Asp Gly Lys Ile Ala Ile 1795 1800 1805			
50	TAC CAC TGG AAC GTG CGA CCG CTG GAA GAA GAC ACC AGT TGG AAT GCA 5472 Tyr His Trp Asn Val Arg Pro Leu Glu Glu Asp Thr Ser Trp Asn Ala 1810 1815 1820			
55	CAA CAA CTG GAC TCC ACC GAT CCA GAT GCT GTA GCC CAA GAT GAT CCG 5520 Gln Gln Leu Asp Ser Thr Asp Pro Asp Ala Val Ala Gln Asp Asp Pro 1825 1830 1835 1840			
60	ATG CAC TAC AAG GTG GCT ACC TTT ATG GCG ACC TTG GAT CTG CTA ATG 5568 Met His Tyr Lys Val Ala Thr Phe Met Ala Thr Leu Asp Leu Leu Met 1845 1850 1855			
65	GCC CGT GGT GAT GCT GCT TAC CGC CAG TTA GAG CGT GAT ACG TTG GCT 5616 Ala Arg Gly Asp Ala Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Ala 1860 1865 1870			
70	GAA GCT AAA ATG TGG TAT ACA CAG GCG CTT AAT CTG TTG GGT GAT GAG 5664 Glu Ala Lys Met Trp Tyr Thr Gln Ala Leu Asn Leu Leu Gly Asp Glu 1875 1880 1885			
75	CCA CAA GTG ATG CTG AGT ACG ACT TGG GCT AAT CCA ACA TTG GGT AAT 5712 Pro Gln Val Met Leu Ser Thr Thr Trp Ala Asn Pro Thr Leu Gly Asn 1890 1895 1900			
80	GCT GCT TCA AAA ACC ACA CAG CAG GTT CGT CAG CAA GTG CTT ACC CAG 5760 Ala Ala Ser Lys Thr Thr Gln Gln Val Arg Gln Gln Val Leu Thr Gln 1905 1910 1915 1920			

	TTG CGT CTC AAT AGC AGG GTA AAA ACC CCG TTG CTA GGA ACA GCC AAT 5308	
	Leu Arg Leu Asn Ser Arg Val Lys Thr Pro Leu Leu Gly Thr Ala Asn	
	1925	1930 1935
5	TCC CTG ACC GCT TTA TTC CTG CCG CAG GAA AAT AGC AAG CTC AAA GGC 5356	
	Ser Leu Thr Ala Leu Phe Leu Pro Gln Glu Asn Ser Lys Leu Lys Gly	
	1940	1945 1950
10	TAC TGG CCG ACA CTG GCG CAG CGT ATG TTT AAT TTA CGT CAT AAT CTG 5904	
	Tyr Trp Arg Thr Leu Ala Gln Arg Met Phe Asn Leu Arg His Asn Leu	
	1955	1960 1965
15	TCG ATT GAC GGC CAG CCG CTC TCC TTG CCG CTG TAT GCT AAA CCG GCT 5352	
	Ser Ile Asp Gly Gln Pro Leu Ser Leu Pro Leu Tyr Ala Lys Pro Ala	
	1970	1975 1980
20	GAT CCA AAA GCT TTA CTG AGT GCG GCG GTT TCA GCT TCT CAA GGG GGA 6000	
	Asp Pro Lys Ala Leu Leu Ser Ala Ala Val Ser Ala Ser Gln Gly Gly	
	1985	1990 1995 2000
	GCC GAC TTG CCG AAG GCG CCG CTG ACT ATT CAC CGC TTC CCT CAA ATG 6048	
	Ala Asp Leu Pro Lys Ala Pro Leu Thr Ile His Arg Phe Pro Gln Met	
	2005	2010 2015
25	CTA GAA GGG GCA CCG GGC TTG GTT AAC CAG CTT ATA CAG TTC GGT AGT 6096	
	Leu Glu Gly Ala Arg Gly Leu Val Asn Gln Leu Ile Gln Phe Gly Ser	
	2020	2025 2030
30	TCA CTA TTG GGG TAC AGT GAG CGT CAG GAT GCG GAA GCT ATG AGT CAA 6144	
	Ser Leu Leu Gly Tyr Ser Glu Arg Gln Asp Ala Glu Ala Met Ser Gln	
	2035	2040 2045
35	CTA CTG CAA ACC CAA GCC AGC GAG TTA ATA CTG ACC AGT ATT CGT ATG 6192	
	Leu Leu Gln Thr Gln Ala Ser Glu Leu Ile Leu Thr Ser Ile Arg Met	
	2050	2055 2060
40	CAG GAT AAC CAA TTG GCA GAG CTG GAT TCG GAA AAA ACC GCC TTG CAA 6240	
	Gln Asp Asn Gln Leu Ala Glu Leu Asp Ser Glu Lys Thr Ala Leu Gln	
	2065	2070 2075 2080
	GTC TCT TTA GCT GGA GTG CAA CAA CCG TTT GAC AGC TAT AGC CAA CTG 6288	
	Val Ser Leu Ala Gly Val Gln Gln Arg Phe Asp Ser Tyr Ser Gln Leu	
	2085	2090 2095
45	TAT GAG GAG AAC ATC AAC GCA GGT GAG CAG CGA GCG CTG GCG TTA CGC 6336	
	Tyr Glu Glu Asn Ile Asn Ala Gly Glu Gln Arg Ala Leu Ala Leu Arg	
	2100	2105 2110
50	TCA GAA TCT GCT ATT GAG TCT CAG GGA GCG CAG ATT TCC CGT ATG GCA 6384	
	Ser Glu Ser Ala Ile Glu Ser Gln Gly Ala Gln Ile Ser Arg Met Ala	
	2115	2120 2125
55	GGC GCG GGT GTT GAT ATG GCA CCA AAT ATC TTC GGC CTG GCT GAT GGC 6432	
	Gly Ala Gly Val Asp Met Ala Pro Asn Ile Phe Gly Leu Ala Asp Gly	
	2130	2135 2140
60	GGC ATG CAT TAT GGT GCT ATT GCC TAT GCC ATC GCT GAC GGT ATT GAG 6480	
	Gly Met His Tyr Gly Ala Ile Ala Tyr Ala Ile Ala Asp Gly Ile Glu	
	2145	2150 2155 2160
	TTG AGT GCT TCT GCC AAG ATG GTT GAT GCG GAG AAA GTT GCT CAG TCG 6528	
	Leu Ser Ala Ser Ala Lys Met Val Asp Ala Glu Lys Val Ala Gln Ser	
	2165	2170 2175
65	GAA ATA TAT CGC CGT CGC CGT CAA GAA TGG AAA ATT CAG CGT GAC AAC 5576	
	Glu Ile Tyr Arg Arg Arg Arg Gln Glu Trp Lys Ile Gln Arg Asp Asn	

	2180	2135	2190
5	GCA CAA GCG GAG ATT AAC CAG TTA AAC GCG CAA CTG GAA TCA CTG TCT 6614 Ala Gln Ala Glu Ile Asn Gln Leu Asn Ala Gln Leu Glu Ser Leu Ser 2195 2200 2205		
10	ATT CGC CGT GAA GCC GCT GAA ATG CAA AAA GAG TAC CTG AAA ACC CAG 6672 Ile Arg Arg Glu Ala Ala Glu Met Gln Lys Glu Tyr Leu Lys Thr Gln 2210 2215 2220		
	CAA GCT CAG GCG CAG GCA CAA CTT ACT TTC TTA AGA AGC AAA TTC AGT 6720 Gln Ala Gln Ala Gln Ala Gln Leu Thr Phe Leu Arg Ser Lys Phe Ser 2225 2230 2235 2240		
15	AAT CAA GCG TTA TAT AGT TGG TTA CGA GCG CGT TTG TCA GGT ATT TAT 6766 Asn Gln Ala Leu Tyr Ser Trp Leu Arg Gly Arg Leu Ser Gly Ile Tyr 2245 2250 2255		
20	TTC CAG TTC TAT GAC TTG GCC GTA TCA CGT TGC CTG ATG GCA GAG CAA 6815 Phe Gln Phe Tyr Asp Leu Ala Val Ser Arg Cys Leu Met Ala Glu Gln 2260 2265 2270		
25	TCC TAT CAA TGG GAA GCT AAT GAT AAT TCC ATT AGC TTT GTC AAA CCG 6864 Ser Tyr Gln Trp Glu Ala Asn Asp Asn Ser Ile Ser Phe Val Lys Pro 2275 2280 2285		
30	GGT GCA TGG CAA GGA ACT TAC GCC GGC TTA TTG TGT GGA GAA GCT TTG 6912 Gly Ala Trp Gln Gly Thr Tyr Ala Gly Leu Leu Cys Gly Glu Ala Leu 2290 2295 2300		
	ATA CAA AAT CTG GCA CAA ATG GAA GAG GCA TAT CTG AAA TGG GAA TCT 6960 Ile Gln Asn Leu Ala Gln Met Glu Glu Ala Tyr Leu Lys Trp Glu Ser 2305 2310 2315 2320		
35	CGC GCT TTG GAA GTA GAA CGC ACG GTT TCA TTG GCA GTG GTT TAT GAT 7006 Arg Ala Leu Glu Val Glu Arg Thr Val Ser Leu Ala Val Val Tyr Asp 2325 2330 2335		
40	TCA CTG GAA GGT AAT GAT CGT TTT AAT TTA GCG GAA CAA ATA CCT GCA 7055 Ser Leu Glu Gly Asn Asp Arg Phe Asn Leu Ala Glu Gln Ile Pro Ala 2340 2345 2350		
45	TTA TTG GAT AAG GGG GAG GGA ACA GCA GGA ACT AAA GAA AAT GCG TTA 7104 Leu Leu Asp Lys Gly Glu Gly Thr Ala Gly Thr Lys Glu Asn Gly Leu 2355 2360 2365		
50	TCA TTG GCT AAT GCT ATC CTG TCA GCT TCG GTC AAA TTG TCC GAC TTG 7152 Ser Leu Ala Asn Ala Ile Leu Ser Ala Ser Val Lys Leu Ser Asp Leu 2370 2375 2380		
	AAA CTG GGA ACG GAT TAT CCA GAC AGT ATC GTT GGT AGC AAC AAG GTT 7200 Lys Leu Gly Thr Asp Tyr Pro Asp Ser Ile Val Gly Ser Asn Lys Val 2385 2390 2395 2400		
55	CGT CGT ATT AAG CAA ATC AGT GTT TCG CTA CCT GCA TTG GTT GGG CCT 7248 Arg Arg Ile Lys Gln Ile Ser Val Ser Leu Pro Ala Leu Val Gly Pro 2405 2410 2415		
60	TAT CAG GAT GTT CAG GCT ATG CTC AGC TAT GGT GGC AGT ACT CAA TTG 7296 Tyr Gln Asp Val Gln Ala Met Leu Ser Tyr Gly Gly Ser Thr Gln Leu 2420 2425 2430		
65	CCG AAA GGT TGT TCA GCG TTG GCT GTG TCT CAT GGT ACC AAT GAT AGT 7344 Pro Lys Gly Cys Ser Ala Leu Ala Val Ser His Gly Thr Asn Asp Ser 2435 2440 2445		

GGT CAG TTC CAG TTG GAT TTC AAT GAC GGC AAA TAC CTG CCA TTT GAA 7392
 Gly Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys Tyr Leu Pro Phe Glu
 2450 2455 2460

5 GGT ATT GCT CTT GAT GAT CAG GGT ACA CTG AAT CTT CAA TTT CCG AAT 7440
 Gly Ile Ala Leu Asp Asp Gln Gly Thr Leu Asn Leu Gln Phe Pro Asn
 2465 2470 2475 2480

10 GCT ACC GAC AAG CAG AAA GCA ATA TTG CAA ACT ATG AGC GAT ATT ATT 7488
 Ala Thr Asp Lys Gln Lys Ala Ile Leu Gln Thr Met Ser Asp Ile Ile
 2485 2490 2495

TTG CAT ATT CGT TAT ACC ATC CGT TAA 7515
 Leu His Ile Arg Tyr Thr Ile Arg *
 15 2500 2505

(2) INFORMATION FOR SEQ ID NO:12:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2505 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

30 Met Gln Asn Ser Leu Ser Ser Thr Ile Asp Thr Ile Cys Gln Lys Leu
 1 5 10 15
 Gln Leu Thr Cys Pro Ala Glu Ile Ala Leu Tyr Pro Phe Asp Thr Phe
 20 25 30
 35 Arg Glu Lys Thr Arg Gly Met Val Asn Trp Gly Glu Ala Lys Arg Ile
 35 40 45
 Tyr Glu Ile Ala Gln Ala Glu Gln Asp Arg Asn Leu Leu His Glu Lys
 40 50 55 60
 Arg Ile Phe Ala Tyr Ala Asn Pro Leu Leu Lys Asn Ala Val Arg Leu
 65 70 75 80
 45 Gly Thr Arg Gln Met Leu Gly Phe Ile Gln Gly Tyr Ser Asp Leu Phe
 85 90 95
 Gly Asn Arg Ala Asp Asn Tyr Ala Ala Pro Gly Ser Val Ala Ser Met
 100 105 110
 50 Phe Ser Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Lys Asn
 115 120 125
 Leu His Asp Ser Ser Ser Ile Tyr Tyr Leu Asp Lys Arg Arg Pro Asp
 130 135 140
 Leu Ala Ser Leu Met Leu Ser Gln Lys Asn Met Asp Glu Glu Ile Ser
 145 150 155 160
 60 Thr Leu Ala Leu Ser Asn Glu Leu Cys Leu Ala Gly Ile Glu Thr Lys
 165 170 175
 Thr Gly Lys Ser Gln Asp Glu Val Met Asp Met Leu Ser Thr Tyr Arg
 180 185 190
 65

Leu Ser Gly Glu Thr Pro Tyr His His Ala Tyr Glu Thr Val Arg Glu
 195 200 205
 5 Ile Val His Glu Arg Asp Pro Gly Phe Arg His Leu Ser Gln Ala Pro
 210 215 220
 Ile Val Ala Ala Lys Leu Asp Pro Val Thr Leu Leu Gly Ile Ser Ser
 225 230 235 240
 10 His Ile Ser Pro Glu Leu Tyr Asn Leu Leu Ile Glu Glu Ile Pro Glu
 245 250 255
 Lys Asp Glu Ala Ala Leu Asp Thr Leu Tyr Lys Thr Asn Phe Gly Asp
 260 265 270
 15 Ile Thr Thr Ala Gln Leu Met Ser Pro Ser Tyr Leu Ala Arg Tyr Tyr
 275 280 285
 Gly Val Ser Pro Glu Asp Ile Ala Tyr Val Thr Thr Ser Leu Ser His
 290 295 300
 Val Gly Tyr Ser Ser Asp Ile Leu Val Ile Pro Leu Val Asp Gly Val
 305 310 315 320
 25 Gly Lys Met Glu Val Val Arg Val Thr Arg Thr Pro Ser Asp Asn Tyr
 325 330 335
 Thr Ser Gln Thr Asn Tyr Ile Glu Leu Tyr Pro Gln Gly Gly Asp Asn
 340 345 350
 30 Tyr Leu Ile Lys Tyr Asn Leu Ser Asn Ser Phe Gly Leu Asp Asp Phe
 355 360 365
 Tyr Leu Gln Tyr Lys Asp Gly Ser Ala Asp Trp Thr Glu Ile Ala His
 370 375 380
 35 Asn Pro Tyr Pro Asp Met Val Ile Asn Gln Lys Tyr Glu Ser Gln Ala
 385 390 395 400
 40 Thr Ile Lys Arg Ser Asp Ser Asp Asn Ile Leu Ser Ile Gly Leu Gln
 405 410 415
 Arg Trp His Ser Gly Ser Tyr Asn Phe Ala Ala Ala Asn Phe Lys Ile
 420 425 430
 45 Asp Gln Tyr Ser Pro Lys Ala Phe Leu Leu Lys Met Asn Lys Ala Ile
 435 440 445
 Arg Leu Leu Lys Ala Thr Gly Leu Ser Phe Ala Thr Leu Glu Arg Ile
 450 455 460
 Val Asp Ser Val Asn Ser Thr Lys Ser Ile Thr Val Glu Val Leu Asn
 465 470 475 480
 55 Lys Val Tyr Arg Val Lys Phe Tyr Ile Asp Arg Tyr Gly Ile Ser Glu
 485 490 495
 Glu Thr Ala Ala Ile Leu Ala Asn Ile Asn Ile Ser Gln Gln Ala Val
 500 505 510
 60 Gly Asn Gln Leu Ser Gln Phe Glu Gln Leu Phe Asn His Pro Pro Leu
 515 520 525
 Asn Gly Ile Arg Tyr Glu Ile Ser Glu Asp Asn Ser Lys His Leu Pro
 530 535 540
 65

Asn Pro Asp Leu Asn Leu Lys Pro Asp Ser Thr Gly Asp Asp Gln Arg
 545 550 555 560
 5 Lys Ala Val Leu Lys Arg Ala Phe Gln Val Asn Ala Ser Glu Leu Tyr
 565 570 575
 Gln Met Leu Leu Ile Thr Asp Arg Lys Glu Asp Gly Val Ile Lys Asn
 580 585 590
 10 Asn Leu Glu Asn Leu Ser Asp Leu Tyr Leu Val Ser Leu Leu Ala Gln
 595 600 605
 Ile His Asn Leu Thr Ile Ala Glu Leu Asn Ile Leu Leu Val Ile Cys
 610 615 620
 15 Gly Tyr Gly Asp Thr Asn Ile Tyr Gln Ile Thr Asp Asp Asn Leu Ala
 625 630 635 640
 Lys Ile Val Glu Thr Leu Leu Trp Ile Thr Gln Trp Leu Lys Thr Gln
 645 650 655
 Lys Trp Thr Val Thr Asp Leu Phe Leu Met Thr Thr Ala Thr Tyr Ser
 660 665 670
 25 Thr Thr Leu Thr Pro Glu Ile Ser Asn Leu Thr Ala Thr Leu Ser Ser
 675 680 685
 Thr Leu His Gly Lys Glu Ser Leu Ile Gly Glu Asp Leu Lys Arg Ala
 690 695 700
 30 Met Ala Pro Cys Phe Thr Ser Ala Leu His Leu Thr Ser Gln Glu Val
 705 710 715 720
 Ala Tyr Asp Leu Leu Leu Trp Ile Asp Gln Ile Gln Pro Ala Gln Ile
 725 730 735
 35 Thr Val Asp Gly Phe Trp Glu Glu Val Gln Thr Thr Pro Thr Ser Leu
 740 745 750
 40 Lys Val Ile Thr Phe Ala Gln Val Leu Ala Gln Leu Ser Leu Ile Tyr
 755 760 765
 Arg Arg Ile Gly Leu Ser Glu Thr Glu Leu Ser Leu Ile Val Thr Gln
 770 775 780
 45 Ser Ser Leu Leu Val Ala Gly Lys Ser Ile Leu Asp His Gly Leu Leu
 785 790 795 800
 Thr Leu Met Ala Leu Glu Gly Phe His Thr Trp Val Asn Gly Leu Gly
 805 810 815
 Gln His Ala Ser Leu Ile Leu Ala Ala Leu Lys Asp Gly Ala Leu Thr
 820 825 830
 55 Val Thr Asp Val Ala Gln Ala Met Asn Lys Glu Glu Ser Leu Leu Gln
 835 840 845
 Met Ala Ala Asn Gln Val Glu Lys Asp Leu Thr Lys Leu Thr Ser Trp
 850 855 860
 60 Thr Gln Ile Asp Ala Ile Leu Gln Trp Leu Gln Met Ser Ser Ala Leu
 865 870 875 880
 Ala Val Ser Pro Leu Asp Leu Ala Gly Met Met Ala Leu Lys Tyr Gly
 885 890 895
 65

	Ile	Asp	His	Asn	Tyr	Ala	Ala	Trp	Gln	Ala	Ala	Ala	Ala	Ala	Leu	Met	
				900					905						910		
5	Ala	Asp	His	Ala	Asn	Gln	Ala	Gln	Lys	Lys	Leu	Asp	Glu	Thr	Phe	Ser	
				915				920					925				
	Lys	Ala	Leu	Cys	Asn	Tyr	Tyr	Ile	Asn	Ala	Val	Val	Asp	Ser	Ala	Ala	
			930				935					940					
10	Gly	Val	Arg	Asp	Arg	Asn	Gly	Leu	Tyr	Thr	Tyr	Leu	Leu	Ile	Asp	Asn	
						950					955					960	
	Gln	Val	Ser	Ala	Asp	Val	Ile	Thr	Ser	Arg	Ile	Ala	Glu	Ala	Ile	Ala	
					965					970					975		
15	Gly	Ile	Gln	Leu	Tyr	Val	Asn	Arg	Ala	Leu	Asn	Arg	Asp	Glu	Gly	Gln	
				980					985					990			
	Leu	Ala	Ser	Asp	Val	Ser	Thr	Arg	Gln	Phe	Phe	Thr	Asp	Trp	Glu	Arg	
20				995				1000					1005				
	Tyr	Asn	Lys	Arg	Tyr	Ser	Thr	Trp	Ala	Gly	Val	Ser	Glu	Leu	Val	Tyr	
				1010			1015					1020					
25	Tyr	Pro	Glu	Asn	Tyr	Val	Asp	Pro	Thr	Gln	Arg	Ile	Gly	Gln	Thr	Lys	
				1025			1030				1035					1040	
	Met	Met	Asp	Ala	Leu	Leu	Gln	Ser	Ile	Asn	Gln	Ser	Gln	Leu	Asn	Ala	
					1045					1050					1055		
30	Asp	Thr	Val	Glu	Asp	Ala	Phe	Lys	Thr	Tyr	Leu	Thr	Ser	Phe	Glu	Gln	
				1060					1065					1070			
	Val	Ala	Asn	Leu	Lys	Val	Ile	Ser	Ala	Tyr	His	Asp	Asn	Val	Asn	Val	
35				1075				1080					1085				
	Asp	Gln	Gly	Leu	Thr	Tyr	Phe	Ile	Gly	Ile	Asp	Gln	Ala	Ala	Pro	Gly	
				1090			1095					1100					
40	Thr	Tyr	Tyr	Trp	Arg	Ser	Val	Asp	His	Ser	Lys	Cys	Glu	Asn	Gly	Lys	
						1110					1115					1120	
	Phe	Ala	Ala	Asn	Ala	Trp	Gly	Glu	Trp	Asn	Lys	Ile	Thr	Cys	Ala	Val	
					1125				1130					1135			
45	Asn	Pro	Trp	Lys	Asn	Ile	Ile	Arg	Pro	Val	Val	Tyr	Met	Ser	Arg	Leu	
				1140				1145						1150			
	Tyr	Leu	Leu	Trp	Leu	Glu	Gln	Gln	Ser	Lys	Lys	Ser	Asp	Asp	Gly	Lys	
50				1155				1160					1165				
	Thr	Thr	Ile	Tyr	Gln	Tyr	Asn	Leu	Lys	Leu	Ala	His	Ile	Arg	Tyr	Asp	
				1170			1175				1180						
55	Gly	Ser	Trp	Asn	Thr	Pro	Phe	Thr	Phe	Asp	Val	Thr	Glu	Lys	Val	Lys	
				1185			1190				1195					1200	
	Asn	Tyr	Thr	Ser	Ser	Thr	Asp	Ala	Ala	Glu	Ser	Leu	Gly	Leu	Tyr	Cys	
					1205					1210					1215		
60	Thr	Gly	Tyr	Gln	Gly	Glu	Asp	Thr	Leu	Leu	Val	Met	Phe	Tyr	Ser	Met	
				1220					1225					1230			
	Gln	Ser	Ser	Tyr	Ser	Ser	Tyr	Thr	Asp	Asn	Asn	Ala	Pro	Val	Thr	Gly	
65				1235				1240					1245				

Leu Tyr Ile Phe Ala Asp Met Ser Ser Asp Asn Met Thr Asn Ala Gin
 1250 1255 1260
 5 Ala Thr Asn Tyr Trp Asn Asn Ser Tyr Pro Gln Phe Asp Thr Val Met
 1265 1270 1275 1280
 Ala Asp Pro Asp Ser Asp Asn Lys Lys Val Ile Thr Arg Arg Val Asn
 1285 1290 1295
 10 Asn Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Thr Ser Asn
 1300 1305 1310
 Ser Asn Tyr Ser Trp Gly Asp His Ser Leu Thr Met Leu Tyr Gly Gly
 1315 1320 1325
 15 Ser Val Pro Asn Ile Thr Phe Glu Ser Ala Ala Glu Asp Leu Arg Leu
 1330 1335 1340
 Ser Thr Asn Met Ala Leu Ser Ile Ile His Asn Gly Tyr Ala Gly Thr
 1345 1350 1355 1360
 Arg Arg Ile Gln Cys Asn Leu Met Lys Gln Tyr Ala Ser Leu Gly Asp
 1365 1370 1375
 25 Lys Phe Ile Ile Tyr Asp Ser Ser Phe Asp Asp Ala Asn Arg Phe Asn
 1380 1385 1390
 Leu Val Pro Leu Phe Lys Phe Gly Lys Asp Glu Asn Ser Asp Asp Ser
 1395 1400 1405
 30 Ile Cys Ile Tyr Asn Glu Asn Pro Ser Ser Glu Asp Lys Lys Trp Tyr
 1410 1415 1420
 Phe Ser Ser Lys Asp Asp Asn Lys Thr Ala Asp Tyr Asn Gly Gly Thr
 1425 1430 1435 1440
 Gln Cys Ile Asp Ala Gly Thr Ser Asn Lys Asp Phe Tyr Tyr Asn Leu
 1445 1450 1455
 40 Gln Glu Ile Glu Val Ile Ser Val Thr Gly Gly Tyr Trp Ser Ser Tyr
 1460 1465 1470
 Lys Ile Ser Asn Pro Ile Asn Ile Asn Thr Gly Ile Asp Ser Ala Lys
 1475 1480 1485
 45 Val Lys Val Thr Val Lys Ala Gly Gly Asp Asp Gln Ile Phe Thr Ala
 1490 1495 1500
 Asp Asn Ser Thr Tyr Val Pro Gln Gln Pro Ala Pro Ser Phe Glu Glu
 1505 1510 1515 1520
 Met Ile Tyr Gln Phe Asn Asn Leu Thr Ile Asp Cys Lys Asn Leu Asn
 1525 1530 1535
 55 Phe Ile Asp Asn Gln Ala His Ile Glu Ile Asp Phe Thr Ala Thr Ala
 1540 1545 1550
 Gln Asp Gly Arg Phe Leu Gly Ala Glu Thr Phe Ile Ile Pro Val Thr
 1555 1560 1565
 60 Lys Lys Val Leu Gly Thr Glu Asn Val Ile Ala Leu Tyr Ser Glu Asn
 1570 1575 1580
 Asn Gly Val Gln Tyr Met Gln Ile Gly Ala Tyr Arg Thr Arg Leu Asn
 1585 1590 1595 1600
 65

Thr Leu Phe Ala Gln Gln Leu Val Ser Arg Ala Asn Arg Gly Ile Asp
 1605 1610 1615
 5 Ala Val Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu Gly
 1620 1625 1630
 Ala Gly Thr Tyr Val Gln Leu Val Leu Asp Lys Tyr Asp Glu Ser Ile
 1635 1640 1645
 10 His Gly Thr Asn Lys Ser Phe Ala Ile Glu Tyr Val Asp Ile Phe Lys
 1650 1655 1660
 Glu Asn Asp Ser Phe Val Ile Tyr Gln Gly Glu Leu Ser Glu Thr Ser
 1665 1670 1675 1680
 15 Gln Thr Val Val Lys Val Phe Leu Ser Tyr Phe Ile Glu Ala Thr Gly
 1685 1690 1695
 20 Asn Lys Asn His Leu Trp Val Arg Ala Lys Tyr Gln Lys Glu Thr Thr
 1700 1705 1710
 Asp Lys Ile Leu Phe Asp Arg Thr Asp Glu Lys Asp Pro His Gly Trp
 1715 1720 1725
 25 Phe Leu Ser Asp Asp His Lys Thr Phe Ser Gly Leu Ser Ser Ala Gln
 1730 1735 1740
 Ala Leu Lys Asn Asp Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ala
 1745 1750 1755 1760
 30 Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro Met Met Met Ala His
 1765 1770 1775
 35 Arg Leu Leu Gln Glu Gln Asn Phe Asp Ala Ala Asn His Trp Phe Arg
 1780 1785 1790
 Tyr Val Trp Ser Pro Ser Gly Tyr Ile Val Asp Gly Lys Ile Ala Ile
 1795 1800 1805
 40 Tyr His Trp Asn Val Arg Pro Leu Glu Glu Asp Thr Ser Trp Asn Ala
 1810 1815 1820
 Gln Gln Leu Asp Ser Thr Asp Pro Asp Ala Val Ala Gln Asp Asp Pro
 1825 1830 1835 1840
 45 Met His Tyr Lys Val Ala Thr Phe Met Ala Thr Leu Asp Leu Leu Met
 1845 1850 1855
 50 Ala Arg Gly Asp Ala Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Ala
 1860 1865 1870
 Glu Ala Lys Met Trp Tyr Thr Gln Ala Leu Asn Leu Leu Gly Asp Glu
 1875 1880 1885
 55 Pro Gln Val Met Leu Ser Thr Thr Trp Ala Asn Pro Thr Leu Gly Asn
 1890 1895 1900
 Ala Ala Ser Lys Thr Thr Gln Gln Val Arg Gln Gln Val Leu Thr Gln
 1905 1910 1915 1920
 60 Leu Arg Leu Asn Ser Arg Val Lys Thr Pro Leu Leu Gly Thr Ala Asn
 1925 1930 1935
 65 Ser Leu Thr Ala Leu Phe Leu Pro Gln Glu Asn Ser Lys Leu Lys Gly
 1940 1945 1950

Tyr Trp Arg Thr Leu Ala Gln Arg Met Phe Asn Leu Arg His Asn Leu
 1955 1960 1965
 5 Ser Ile Asp Gly Gln Pro Leu Ser Leu Pro Leu Tyr Ala Lys Pro Ala
 1970 1975 1980
 Asp Pro Lys Ala Leu Leu Ser Ala Ala Val Ser Ala Ser Gln Gly Gly
 1985 1990 1995 2000
 10 Ala Asp Leu Pro Lys Ala Pro Leu Thr Ile His Arg Phe Pro Gln Met
 2005 2010 2015
 Leu Glu Gly Ala Arg Gly Leu Val Asn Gln Leu Ile Gln Phe Gly Ser
 2020 2025 2030
 15 Ser Leu Leu Gly Tyr Ser Glu Arg Gln Asp Ala Glu Ala Met Ser Gln
 2035 2040 2045
 Leu Leu Gln Thr Gln Ala Ser Glu Leu Ile Leu Thr Ser Ile Arg Met
 2050 2055 2060
 Gln Asp Asn Gln Leu Ala Glu Leu Asp Ser Glu Lys Thr Ala Leu Gln
 2065 2070 2075 2080
 25 Val Ser Leu Ala Gly Val Gln Gln Arg Phe Asp Ser Tyr Ser Gln Leu
 2085 2090 2095
 Tyr Glu Glu Asn Ile Asn Ala Gly Glu Gln Arg Ala Leu Ala Leu Arg
 2100 2105 2110
 30 Ser Glu Ser Ala Ile Glu Ser Gln Gly Ala Gln Ile Ser Arg Met Ala
 2115 2120 2125
 Gly Ala Gly Val Asp Met Ala Pro Asn Ile Phe Gly Leu Ala Asp Gly
 2130 2135 2140
 Gly Met His Tyr Gly Ala Ile Ala Tyr Ala Ile Ala Asp Gly Ile Glu
 2145 2150 2155 2160
 40 Leu Ser Ala Ser Ala Lys Met Val Asp Ala Glu Lys Val Ala Gln Ser
 2165 2170 2175
 Glu Ile Tyr Arg Arg Arg Arg Gln Glu Trp Lys Ile Gln Arg Asp Asn
 2180 2185 2190
 45 Ala Gln Ala Glu Ile Asn Gln Leu Asn Ala Gln Leu Glu Ser Leu Ser
 2195 2200 2205
 Ile Arg Arg Glu Ala Ala Glu Met Gln Lys Glu Tyr Leu Lys Thr Gln
 2210 2215 2220
 Gln Ala Gln Ala Gln Ala Gln Leu Thr Phe Leu Arg Ser Lys Phe Ser
 2225 2230 2235 2240
 55 Asn Gln Ala Leu Tyr Ser Trp Leu Arg Gly Arg Leu Ser Gly Ile Tyr
 2245 2250 2255
 Phe Gln Phe Tyr Asp Leu Ala Val Ser Arg Cys Leu Met Ala Glu Gln
 2260 2265 2270
 60 Ser Tyr Gln Trp Glu Ala Asn Asp Asn Ser Ile Ser Phe Val Lys Pro
 2275 2280 2285
 Gly Ala Trp Gln Gly Thr Tyr Ala Gly Leu Leu Cys Gly Glu Ala Leu
 2290 2295 2300
 65

Ile Gln Asn Leu Ala Gln Met Glu Glu Ala Tyr Leu Lys Trp Glu Ser
2305 2310 2315 2320

5 Arg Ala Leu Glu Val Glu Arg Thr Val Ser Leu Ala Val Val Tyr Asp
2325 2330 2335

Ser Leu Glu Gly Asn Asp Arg Phe Asn Leu Ala Glu Gln Ile Pro Ala
2340 2345 2350

10 Leu Leu Asp Lys Gly Glu Gly Thr Ala Gly Thr Lys Glu Asn Gly Leu
2355 2360 2365

Ser Leu Ala Asn Ala Ile Leu Ser Ala Ser Val Lys Leu Ser Asp Leu
2370 2375 2380

15 Lys Leu Gly Thr Asp Tyr Pro Asp Ser Ile Val Gly Ser Asn Lys Val
2385 2390 2395 2400

20 Arg Arg Ile Lys Gln Ile Ser Val Ser Leu Pro Ala Leu Val Gly Pro
2405 2410 2415

Tyr Gln Asp Val Gln Ala Met Leu Ser Tyr Gly Gly Ser Thr Gln Leu
2420 2425 2430

25 Pro Lys Gly Cys Ser Ala Leu Ala Val Ser His Gly Thr Asn Asp Ser
2435 2440 2445

Gly Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys Tyr Leu Pro Phe Glu
2450 2455 2460

30 Gly Ile Ala Leu Asp Asp Gln Gly Thr Leu Asn Leu Gln Phe Pro Asn
2465 2470 2475 2480

35 Ala Thr Asp Lys Gln Lys Ala Ile Leu Gln Thr Met Ser Asp Ile Ile
2485 2490 2495

Leu His Ile Arg Tyr Thr Ile Arg *
2500 2505

40

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Ile Gly Tyr Asn Asn Gln Phe Ser Gly Xaa Ala
1 5 10

55

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gln Asn Ser Gln Thr Phe Ser Val Gly Glu Leu
1 5 10

10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

25

Ala Gln Asp Gly Asn Gln Asp Thr Phe Phe Ser Gly Asn Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Gln Asn Ser Leu
1 5

45 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: peptide

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala Phe Asn Ile Asp Asp Val Ser Leu Phe
1 5 10

60

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn Ser Ser Asn
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Ser Asp Leu Val Thr Thr Ser Pro Leu Ser Glu Ala Ile Gly Ser
 1 5 10 15

Leu Gln Leu Phe Ile
 20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Tyr Tyr Ile Gln Ala Gln Gln Leu Leu Gly Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Ile Asp Ala Val Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro
1 5 10 15

10 Gln Leu Gly Ala Gly Thr Tyr Val Gln Leu
20 25

(2) INFORMATION FOR SEQ ID NO:22:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Ser Asn Pro Ile Asn Ile Asn Thr Gly Ile Asp Ser Ala Lys
1 5 10 15

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
35 (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

45 Thr Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Val Leu Gly Thr Glu Asn Val Ile Ala Leu Tyr Ser Glu Asn Asn Gly

1 5 10 15
 Val Gln Tyr Met Gln Ile
 20

5

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 6005 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: RBS
 (B) LOCATION: 1..9

20

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 16..3585
 (D) OTHER INFORMATION: /product= "P8"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

30 AAGAAGGAAT TGATT ATG TCT GAA TCT TTA TTT ACA CAA ACG TTG AAA GAA 51
 Met Ser Glu Ser Leu Phe Thr Gln Thr Leu Lys Glu
 1 5 10

35 GCG CGC CGT GAT GCA TTG GTT GCT CAT TAT ATT GCT ACT CAG GTG CCC 99
 Ala Arg Arg Asp Ala Leu Val Ala His Tyr Ile Ala Thr Gln Val Pro
 15 20 25

40 GCA GAT TTA AAA GAG AGT ATC CAG ACC GCG GAT GAT CTG TAC GAA TAT 147
 Ala Asp Leu Lys Glu Ser Ile Gln Thr Ala Asp Asp Leu Tyr Glu Tyr
 30 35 40

45 CTG TTG CTG GAT ACC AAA ATT AGC GAT CTG GTT ACT ACT TCA CCG CTG 195
 Leu Leu Leu Asp Thr Lys Ile Ser Asp Leu Val Thr Thr Ser Pro Leu
 45 50 60

50 TCC GAA GCG ATT GGC AGT CTG CAA TTG TTT ATT CAT CGT GCG ATA GAG 243
 Ser Glu Ala Ile Gly Ser Leu Gln Leu Phe Ile His Arg Ala Ile Glu
 65 70 75

55 GGC TAT GAC GGC ACG CTG GCA GAC TCA GCA AAA CCC TAT TTT GCC GAT 291
 Gly Tyr Asp Gly Thr Leu Ala Asp Ser Ala Lys Pro Tyr Phe Ala Asp
 80 85 90

60 GAA CAG TTT TTA TAT AAC TGG GAT AGT TTT AAC CAC CGT TAT AGC ACT 339
 Glu Gln Phe Leu Tyr Asn Trp Asp Ser Phe Asn His Arg Tyr Ser Thr
 95 100 105

TGG GCT GGC AAG GAA CGG TTG AAA TTC TAT GCC GGG GAT TAT ATT GAT 387
 Trp Ala Gly Lys Glu Arg Leu Lys Phe Tyr Ala Gly Asp Tyr Ile Asp
 110 115 120

CCA ACA TTG CGA TTG AAT AAG ACC GAG ATA TTT ACC GCA TTT GAA CAA 435
 Pro Thr Leu Arg Leu Asn Lys Thr Glu Ile Phe Thr Ala Phe Glu Gln
 125 130 135 140

	CGT ATT TCT CAA GGG AAA TTA AAA AGT GAA TTA GTC GAA TCT AAA TTA	433
	Gly Ile Ser Gln Gly Lys Leu Lys Ser Glu Leu Val Glu Ser Lys Leu	
	145 150 155	
5	CGT GAT TAT CTA ATT AGT TAT GAC ACT TTA GCC ACC CTT GAT TAT ATT	531
	Arg Asp Tyr Leu Ile Ser Tyr Asp Thr Leu Ala Thr Leu Asp Tyr Ile	
	160 165 170	
10	ACT GCC TGC CAA GGC AAA GAT AAT AAA ACC ATC TTC TTT ATT GGC CGT	579
	Thr Ala Cys Gln Gly Lys Asp Asn Lys Thr Ile Phe Phe Ile Gly Arg	
	175 180 185	
15	ACA CAG AAT GCA CCC TAT GCA TTT TAT TGG CGA AAA TTA ACT TTA GTC	627
	Thr Gln Asn Ala Pro Tyr Ala Phe Tyr Trp Arg Lys Leu Thr Leu Val	
	190 195 200	
20	ACT GAT GGC GGT AAG TTG AAA CCA GAT CAA TGG TCA GAG TGG CGA GCA	675
	Thr Asp Gly Gly Lys Leu Lys Pro Asp Gln Trp Ser Glu Trp Arg Ala	
	205 210 215 220	
25	ATT AAT GCC GGG ATT AGT GAG GCA TAT TCA GGG CAT GTC GAG CCT TTC	723
	Ile Asn Ala Gly Ile Ser Glu Ala Tyr Ser Gly His Val Glu Pro Phe	
	225 230 235	
30	TGG GAA AAT AAC AAG CTG CAC ATC CGT TGG TTT ACT ATC TCG AAA GAA	771
	Trp Glu Asn Asn Lys Leu His Ile Arg Trp Phe Thr Ile Ser Lys Glu	
	240 245 250	
35	GAT AAA ATA GAT TTT GTT TAT AAA AAC ATC TGG GTG ATG AGT AGC GAT	819
	Asp Lys Ile Asp Phe Val Tyr Lys Asn Ile Trp Val Met Ser Ser Asp	
	255 260 265	
40	TAT AGC TGG GCA TCA AAG AAA AAA ATC TTG GAA CTT TCT TTT ACT GAC	867
	Tyr Ser Trp Ala Ser Lys Lys Lys Ile Leu Glu Leu Ser Phe Thr Asp	
	270 275 280	
45	TAC AAT AGA GTT GGA GCA ACA GGA TCA TCA AGC CCG ACT GAA GTA GCT	915
	Tyr Asn Arg Val Gly Ala Thr Gly Ser Ser Ser Pro Thr Glu Val Ala	
	285 290 295 300	
50	TCA CAA TAT GGT TCT GAT GCT CAG ATG AAT ATT TCT GAT GAT GGG ACT	963
	Ser Gln Tyr Gly Ser Asp Ala Gln Met Asn Ile Ser Asp Asp Gly Thr	
	305 310 315	
55	GTA CTT ATT TTT CAG AAT GCC GGC GGA GCT ACT CCC AGT ACT GGA GTG	1011
	Val Leu Ile Phe Gln Asn Ala Gly Gly Ala Thr Pro Ser Thr Gly Val	
	320 325 330	
60	ACG TTA TGT TAT GAC TCT GGC AAC GTG ATT AAG AAC CTA TCT AGT ACA	1059
	Thr Leu Cys Tyr Asp Ser Gly Asn Val Ile Lys Asn Leu Ser Ser Thr	
	335 340 345	
65	GGA AGT GCA AAT TTA TCG TCA AAG GAT TAT GCC ACA ACT AAA TTA CGC	1107
	Gly Ser Ala Asn Leu Ser Ser Lys Asp Tyr Ala Thr Thr Lys Leu Arg	
	350 355 360	
70	ATG TGT CAT GGA CAA AGT TAC AAT GAT AAT AAC TAC TGC AAT TTT ACA	1155
	Met Cys His Gly Gln Ser Tyr Asn Asp Asn Asn Tyr Cys Asn Phe Thr	
	365 370 375 380	
75	CTC TCT ATT AAT ACA ATA GAA TTC ACC TCC TAC GGC ACA TTC TCA TCA	1203
	Leu Ser Ile Asn Thr Ile Glu Phe Thr Ser Tyr Gly Thr Phe Ser Ser	
	385 390 395	
80	GAT GGA AAA CAA TTT ACA CCA CCT TCT GGT TCT GCC ATT GAT TTA CAC	1251
	Asp Gly Lys Gln Phe Thr Pro Pro Ser Gly Ser Ala Ile Asp Leu His	

	400	405	410	
5	CTC CCT AAT TAT GTA GAT CTC AAC GCG CTA TTA GAT ATT AGC CTC GAT 1299 Leu Pro Asn Tyr Val Asp Leu Asn Ala Leu Leu Asp Ile Ser Leu Asp 415 420 425			
10	TCA CTA CTT AAT TAT GAC GTT CAG GGG CAG TTT GGC GGA TCT AAT CCG 1347 Ser Leu Leu Asn Tyr Asp Val Gln Gly Gln Phe Gly Gly Ser Asn Pro 430 435 440			
15	GTT GAT AAT TTC ACT GGT CCC TAT GGT ATT TAT CTA TGG GAA ATC TTC 1395 Val Asp Asn Phe Ser Gly Pro Tyr Gly Ile Tyr Leu Trp Glu Ile Phe 445 450 455 460			
20	TTC CAT ATT CCG TTC CTT GTT ACG GTC CGT ATG CAA ACC GAA CAA CGT 1443 Phe His Ile Pro Phe Leu Val Thr Val Arg Met Gln Thr Glu Gln Arg 465 470 475			
25	TAC GAA GAC GCG GAC ACT TGG TAC AAA TAT ATT TTC CGC AGC GCC GGT 1491 Tyr Glu Asp Ala Asp Thr Trp Tyr Lys Tyr Ile Phe Arg Ser Ala Gly 480 485 490			
30	TAT CGC GAT GCT AAT GGC CAG CTC ATT ATG GAT GGC AGT AAA CCA CGT 1539 Tyr Arg Asp Ala Asn Gly Gln Leu Ile Met Asp Gly Ser Lys Pro Arg 495 500 505			
35	TAT TGG AAT GTG ATG CCA TTG CAA CTG GAT ACC GCA TGG GAT ACC ACA 1587 Tyr Trp Asn Val Met Pro Leu Gln Leu Asp Thr Ala Trp Asp Thr Thr 510 515 520			
40	CAG CCC GCC ACC ACT GAT CCA GAT GTG ATC GCT ATG GCG GAC CCG ATG 1635 Gln Pro Ala Thr Thr Asp Pro Asp Val Ile Ala Met Ala Asp Pro Met 525 530 535 540			
45	CAT TAC AAG CTG GCG ATA TTC CTG CAT ACC CTT GAT CTA TTG ATT GCC 1683 His Tyr Lys Leu Ala Ile Phe Leu His Thr Leu Asp Leu Leu Ile Ala 545 550 555			
50	CGA GGC GAC AGC GCT TAC CGT CAA CTT GAA CGC GAT ACT CTA GTC GAA 1731 Arg Gly Asp Ser Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Val Glu 560 565 570			
55	GCC AAA ATG TAC TAC ATT CAG GCA CAA CAG CTA CTG GGA CCG CGC CCT 1779 Ala Lys Met Tyr Tyr Ile Gln Ala Gln Gln Leu Leu Gly Pro Arg Pro 575 580 585			
60	GAT ATC CAT ACC ACC AAT ACT TGG CCA AAT CCC ACC TTG AGT AAA GAA 1827 Asp Ile His Thr Thr Asn Thr Trp Pro Asn Pro Thr Leu Ser Lys Glu 590 595 600			
65	GCT GGC GCT ATT GCC ACA CCG ACA TTC CTC AGT TCA CCG GAG GTG ATG 1875 Ala Gly Ala Ile Ala Thr Pro Thr Phe Leu Ser Ser Pro Glu Val Met 605 610 615 620			
70	ACG TTC GCT GCC TGG CTA AGC GCA GGC GAT ACC GCA AAT ATT GGC GAC 1923 Thr Phe Ala Ala Trp Leu Ser Ala Gly Asp Thr Ala Asn Ile Gly Asp 625 630 635			
75	GGT GAT TTC TTG CCA CCG TAC AAC GAT GTA CTA CTC GGT TAC TGG GAT 1971 Gly Asp Phe Leu Pro Pro Tyr Asn Asp Val Leu Leu Gly Tyr Trp Asp 640 645 650			
80	AAA CTT GAG TTA CGC CTA TAC AAC CTG CGC CAC AAT CTG AGT CTG GAT 2019 Lys Leu Glu Leu Arg Leu Tyr Asn Leu Arg His Asn Leu Ser Leu Asp 655 660 665			

	GGT CAA CCG CTA AAT CTG CCA CTG TAT GCC ACG CCG GTA GAC CCG AAA 2057
	Gly Gln Pro Leu Asn Leu Pro Leu Tyr Ala Thr Pro Val Asp Pro Lys
	570 675 680
5	ACC CTG CAA CGC CAG CAA GCC GGA GGG GAC GGT ACA GGC AGT AGT CCG 2115
	Thr Leu Gln Arg Gln Gln Ala Gly Gly Asp Gly Thr Gly Ser Ser Pro
	685 690 695 700
10	GCT GGT GGT CAA GGC AGT GTT CAG GGC TGG CGC TAT CCG TTA TTG GTA 2153
	Ala Gly Gly Gln Gly Ser Val Gln Gly Trp Arg Tyr Pro Leu Leu Val
	705 710 715
15	GAA CGC GCC CGC TCT GCC GTG AGT TTG TTG ACT CAG TTC GGC AAC AGC 2211
	Glu Arg Ala Arg Ser Ala Val Ser Leu Thr Gln Phe Gly Asn Ser
	720 725 730
20	TTA CAA ACA ACG TTA GAA CAT CAG GAT AAT GAA AAA ATG ACG ATA CTG 2259
	Leu Gln Thr Thr Leu Glu His Gln Asp Asn Glu Lys Met Thr Ile Leu
	735 740 745
	TTG CAG ACT CAA CAG GAA GCC ATC CTG AAA CAT CAG CAC GAT ATA CAA 2307
	Leu Gln Thr Gln Gln Glu Ala Ile Leu Lys His Gln His Asp Ile Gln
	750 755 760
25	CAA AAT AAT CTA AAA GGA TTA CAA CAC AGC CTG ACC GCA TTA CAG GCT 2355
	Gln Asn Asn Leu Lys Gly Leu Gln His Ser Leu Thr Ala Leu Gln Ala
	765 770 775 780
30	AGC CGT GAT GGC GAC ACA TTG CGG CAA AAA CAT TAC AGC GAC CTG ATT 2403
	Ser Arg Asp Gly Asp Thr Leu Arg Gln Lys His Tyr Ser Asp Leu Ile
	785 790 795
35	AAC GGT GGT CTA TCT GCG GCA GAA ATC GCC GGT CTG ACA CTA CGC AGC 2451
	Asn Gly Gly Leu Ser Ala Ala Glu Ile Ala Gly Leu Thr Leu Arg Ser
	800 805 810
40	ACC GCC ATG ATT ACC AAT GGC GTT GCA ACG GGA TTG CTG ATT GCC GGC 2499
	Thr Ala Met Ile Thr Asn Gly Val Ala Thr Gly Leu Leu Ile Ala Gly
	815 820 825
	GGA ATC GCC AAC GCG GTA CCT AAC GTC TTC GGG CTG GCT AAC GGT GGA 2547
	Gly Ile Ala Asn Ala Val Pro Asn Val Phe Gly Leu Ala Asn Gly Gly
	830 835 840
45	TCG GAA TGG GGA GCG CCA TTA ATT GGC TCC GGG CAA GCA ACC CAA GTT 2595
	Ser Glu Trp Gly Ala Pro Leu Ile Gly Ser Gly Gln Ala Thr Gln Val
	845 850 855 860
50	GGC GCC GGC ATC CAG GAT CAG AGC GCG GGC ATT TCA GAA GTG ACA GCA 2643
	Gly Ala Gly Ile Gln Asp Gln Ser Ala Gly Ile Ser Glu Val Thr Ala
	865 870 875
55	GGC TAT CAG CGT CGT CAG GAA GAA TGG GCA TTG CAA CGG GAT ATT GCT 2691
	Gly Tyr Gln Arg Arg Gln Glu Glu Trp Ala Leu Gln Arg Asp Ile Ala
	880 885 890
60	GAT AAC GAA ATA ACC CAA CTG GAT GCC CAG ATA CAA AGC CTG CAA GAG 2739
	Asp Asn Glu Ile Thr Gln Leu Asp Ala Gln Ile Gln Ser Leu Gln Glu
	895 900 905
	CAA ATC ACG ATG GCA CAA AAA CAG ATC ACG CTC TCT GAA ACC GAA CAA 2787
	Gln Ile Thr Met Ala Gln Lys Gln Ile Thr Leu Ser Glu Thr Glu Gln
	910 915 920
65	GCG AAT GCC CAA GCG ATT TAT GAC CTG CAA ACC ACT CGT TTT ACC GGG 2835
	Ala Asn Ala Gln Ala Ile Tyr Asp Leu Gln Thr Thr Arg Phe Thr Gly

	925	930	935	940	
5	CAG GCA CTG TAT AAC TGG ATG GCC GGT CGT CTC TCC GCG CTC TAT TAC 2333 Gln Ala Leu Tyr Asn Trp Met Ala Gly Arg Leu Ser Ala Leu Tyr Tyr 945 950 955				
10	CAA ATG TAT GAT TCC ACT CTG CCA ATC TGT CTC CAG CCA AAA GCC GCA 2931 Gln Met Tyr Asp Ser Thr Leu Pro Ile Cys Leu Gln Pro Lys Ala Ala 960 965 970				
	TTA GTA CAG GAA TTA GGC GAG AAA GAG AGC GAC AGT CTT TTC CAG GTT 2979 Leu Val Gln Glu Leu Gly Glu Lys Glu Ser Asp Ser Leu Phe Gln Val 975 980 985				
15	CCG GTG TGG AAT GAT CTG TGG CAA GGG CTG TTA GCA GGA GAA GGT TTA 3027 Pro Val Trp Asn Asp Leu Trp Gln Gly Leu Leu Ala Gly Glu Gly Leu 990 995 1000				
20	AGT TCA GAG CTA CAG AAA CTG GAT GCC ATC TGG CTT GCA CGT GGT GGT 3075 Ser Ser Glu Leu Gln Lys Leu Asp Ala Ile Trp Leu Ala Arg Gly Gly 1005 1010 1015 1020				
25	ATT GGG CTA GAA GCC ATC CGC ACC GTG TCG CTG GAT ACC CTG TTT GGC 3123 Ile Gly Leu Glu Ala Ile Arg Thr Val Ser Leu Asp Thr Leu Phe Gly 1025 1030 1035				
30	ACA GGG ACG TTA AGT GAA AAT ATC AAT AAA GTG CTT AAC GGG GAA ACG 3171 Thr Gly Thr Leu Ser Glu Asn Ile Asn Lys Val Leu Asn Gly Glu Thr 1040 1045 1050				
	GTA TCT CCA TCC GGT GGC GTC ACT CTG GCG CTG ACA GGG GAT ATC TTC 3219 Val Ser Pro Ser Gly Gly Val Thr Leu Ala Leu Thr Gly Asp Ile Phe 1055 1060 1065				
35	CAA GCA ACA CTG GAT TTG AGT CAG CTA GGT TTG GAT AAC TCT TAC AAC 3267 Gln Ala Thr Leu Asp Leu Ser Gln Leu Gly Leu Asp Asn Ser Tyr Asn 1070 1075 1080				
40	TTG GGT AAC GAG AAG AAA CGT CGT ATT AAA CGT ATC GCC GTC ACC CTG 3315 Leu Gly Asn Glu Lys Lys Arg Arg Ile Lys Arg Ile Ala Val Thr Leu 1085 1090 1095 1100				
45	CCA ACA CTT CTG GGG CCA TAT CAA GAT CTT GAA GCC ACA CTG GTA ATG 3363 Pro Thr Leu Leu Gly Pro Tyr Gln Asp Leu Glu Ala Thr Leu Val Met 1105 1110 1115				
50	GGT GCG GAA ATC GCC GCC TTA TCA CAC GGT GTG AAT GAC GGA GGC CGG 3411 Gly Ala Glu Ile Ala Ala Leu Ser His Gly Val Asn Asp Gly Gly Arg 1120 1125 1130				
	TTT GTT ACC GAC TTT AAC GAC AGC CGT TTT CTG CCT TTT GAA GGT CGA 3459 Phe Val Thr Asp Phe Asn Asp Ser Arg Phe Leu Pro Phe Glu Gly Arg 1135 1140 1145				
55	GAT GCA ACA ACC GGC ACA CTG GAG CTC AAT ATT TTC CAT GCG GGT AAA 3507 Asp Ala Thr Thr Gly Thr Leu Glu Leu Asn Ile Phe His Ala Gly Lys 1150 1155 1160				
60	GAG GGA ACG CAA CAC GAG TTG GTC GCG AAT CTG AGT GAC ATC ATT GTG 3555 Glu Gly Thr Gln His Glu Leu Val Ala Asn Leu Ser Asp Ile Ile Val 1165 1170 1175 1180				
65	CAT CTG AAT TAC ATC ATT CGA GAC GCG TAA ATTTCTTTTC TTTGTCGATT 3605 His Leu Asn Tyr Ile Ile Arg Asp Ala 1185 1190				

ACAGGTCCCT ATCAGGGGCC TGTATTAAAG GAGTACTTTA TGCAGGATTC ACCAGAAGTA 3555
TCGATTACAA CGCTGTCACT TCCCAAAGGT GCGGGTGCTA TCAATGGCAT GGGAGAAGCA 3725
5 CTGAATGCTG CCGGCCCTGA TGGAAATGGCC TCCCTATCTC TGCCATTACC CCTTTCGACC 3785
GGCAGAGGGA CGGCTCCTGG ATTATCGCTG ATTTACAGCA ACAGTGCAGG TAATGGGCCT 3845
10 TTCGGCATCG GCTGGCAATG CCGGTGTTATG TCCATTAGCC GACGCACCCA ACATGGCATT 3905
CCACAATACG GTAATGACGA CACGTTCTTA TCCCCACAAG GCGAGGTCAT GAATATCGCC 3965
CTGAATGACC AAGGGCAACC TGATATCCGT CAAGACGTTA AAACGCTGCA AGGCGTTACC 4025
15 TTGCCAATTT CCTATACCST GACCCGCTAT CAAGCCCGCC AGATCCTGGA TTTCAGTAA 4085
ATCGAATACT GGCAACCTGC CTCCGGTCAA GAAGGACGCG CTTTCTGGCT GATATCGACA 4145
CCGGACGGGC ATCTACACAT CTTAGGGAAA ACCGCGCAGG CTTGTCTGGC AAATCCGCAA 4205
20 AATGACCAAC AAATCGCCCA GTGGTTGCTG GAAGAACTG TGACGCCAGC CCGTGAACAT 4265
GTCAGCTATC AATATCGAGC CGAAGATGAA GCCCATTTGTG ACGACAATGA AAAAACCCT 4325
25 CATCCCAATG TTACCGCACA GCGCTATCTG GTACAGGTGA ACTACAGGCA ACATCAAACC 4385
ACAAGCCAGC CTGTTCTGTAC TGGATAACGC ACCTCCCGCA CCGGAAGAGT GGCTGTTTCA 4445
TCTGGTCTTT GACCACGGTG AGCGCGTACC TCACTTCATA CCGTGCCAAC ATGGGATGCA 4505
30 GGTACAGCGC AATGGTCTGT ACGCCCGGAT ATCTTCTCTC GCTATGAATA TGGTTTTGAA 4565
GTGCGTACTC GCCGCTTATG TCAACAAGTG CTGATGTTTC ACCGCACCGC GCTCATGGCC 4625
35 GGAGAAGCCA GTACCAATGA CGCCCCGAA CTGGTTGGAC GCTTAATACT GGAATATGAC 4685
AAAAACGCCA GCGTCACCAC GTTGATTACC ATCCGTCAAT TAAGCCATGA ATCGGACGGG 4745
AGGCCAGTCA CCCAGCCACC ACTAGAACTA GCCTGGCAAC GGTTTGATCT GGAGAAAATC 4805
40 CCGACATGGC AACGCTTTGA CGCACTAGAT AATTTTAACT CGCAGCAACG TTATCAACTG 4865
GTTGATCTGC GGGGAGAAGG GTTGCCAGGT ATGCTGTATC AAGATCGAGG CGCTTGGTGG 4925
45 TATAAAGCTC CGCAACGTCA GGAAGACGGA GACAGCAATG CCGTCACTTA CGACAAAATC 4985
GCCCCACTGC CTACCCTACC CAATTTGCAG GATAATGCCT CATTGATGGA TATCAACGGA 5045
GACGGCCAAC TGGATTGGGT TGTACCAGCC TCCGGTATTC GCGGATACCA TAGTCAGCAA 5105
50 CCCGATGGAA AGTGGACGCA CTTTACGCCA ATCAATGCCT TGCCCGTGGA ATATTTTCAT 5165
CCAAGCATCC AGTTCGCTGA CCTTACCGGG GCAGGCTTAT CTGATTTAGT GTTGATCGGG 5225
55 CCGAAAAGCG TCGTCTATA TGCCAACCAG CGAAACGGCT GCGGTAAAGG AGAAGATGTC 5285
CCCCAATCCA CAGGTATCAC CCTGCCTGTC ACAGGGACCG ATGCCCCGAA ACTGGTGGCT 5345
TTCAGTGATA TGCTCGGTTT CCGTCAACAA CATCTGGTGG AAATCAAGGG TAATCGCGTC 5405
60 ACCTGTTGGC CGAATCTAGG GCATGGCCGT TTCGGTCAAC CACTAACTCT GTCAGGATTT 5465
AGCCAGCCCG AAAATAGCTT CAATCCCGAA CGGCTGTTTC TGGCGGATAT CGACGGCTCC 5525
65 GGCACCACCG ACCTTATCTA TCGCAATCC GGCTCTTTGC TCATTTATCT CAACCAAAGT 5585

5 GTTATCAGT TTGATGCCCC GTTGACATTA GCGTTGCCAG AAGGCGTACA ATTTGACAAAC 5645
 ACTTGCCAAC TTCAAGTCGC CGATATTCAG GGATTAGGGA TAGCCAGCTT GATTCTGACT 5705
 10 GTGCCACATA TCGCGCCACA TCACTGGCGT TGTGACCTGT CACTGACCAA ACCCTGGTTG 5765
 TTGAATGTAA TGAACAATAA CCGGGGCGCA CATCACACGC TACATTATCG TAGTTCCGCG 5825
 CAATTCTCGT TGGATGAAAA ATTACAGCTC ACCAAAGCAG GCAAATCTCC GGCTTGTTAT 5885
 CTGCCGTTTC CAATGCATTT GCTATGGTAT ACCGAAATTC AGGATGAAAT CAGCGGCAAC 5945
 CGGCTCACCA GTGAAGTCAA CTACAGCCAC GCGCTCTGGG ATGGTAAAGA GCGGGAATTC 6005

15

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1190 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ser Glu Ser Leu Phe Thr Gln Thr Leu Lys Glu Ala Arg Arg Asp
 1 5 10 15
 30 Ala Leu Val Ala His Tyr Ile Ala Thr Gln Val Pro Ala Asp Leu Lys
 20 25 30
 35 Glu Ser Ile Gln Thr Ala Asp Asp Leu Tyr Glu Tyr Leu Leu Leu Asp
 35 40 45
 Thr Lys Ile Ser Asp Leu Val Thr Thr Ser Pro Leu Ser Glu Ala Ile
 50 55 60
 40 Gly Ser Leu Gln Leu Phe Ile His Arg Ala Ile Glu Gly Tyr Asp Gly
 65 70 75 80
 Thr Leu Ala Asp Ser Ala Lys Pro Tyr Phe Ala Asp Glu Gln Phe Leu
 85 90 95
 45 Tyr Asn Trp Asp Ser Phe Asn His Arg Tyr Ser Thr Trp Ala Gly Lys
 100 105 110
 50 Glu Arg Leu Lys Phe Tyr Ala Gly Asp Tyr Ile Asp Pro Thr Leu Arg
 115 120 125
 Leu Asn Lys Thr Glu Ile Phe Thr Ala Phe Glu Gln Gly Ile Ser Gln
 130 135 140
 55 Gly Lys Leu Lys Ser Glu Leu Val Glu Ser Lys Leu Arg Asp Tyr Leu
 145 150 155 160
 Ile Ser Tyr Asp Thr Leu Ala Thr Leu Asp Tyr Ile Thr Ala Cys Gln
 165 170 175
 60 Gly Lys Asp Asn Lys Thr Ile Phe Phe Ile Gly Arg Thr Gln Asn Ala
 180 185 190
 65 Pro Tyr Ala Phe Tyr Trp Arg Lys Leu Thr Leu Val Thr Asp Gly Gly
 195 200 205

Lys Leu Lys Pro Asp Gln Trp Ser Glu Trp Arg Ala Ile Asn Ala Gly
 210 215 220
 5 Ile Ser Glu Ala Tyr Ser Gly His Val Glu Pro Phe Trp Glu Asn Asn
 225 230 235 240
 Lys Leu His Ile Arg Trp Phe Thr Ile Ser Lys Glu Asp Lys Ile Asp
 245 250 255
 10 Phe Val Tyr Lys Asn Ile Trp Val Met Ser Ser Asp Tyr Ser Trp Ala
 260 265 270
 Ser Lys Lys Lys Ile Leu Glu Leu Ser Phe Thr Asp Tyr Asn Arg Val
 275 280 285
 Gly Ala Thr Gly Ser Ser Ser Pro Thr Glu Val Ala Ser Gln Tyr Gly
 290 295 300
 20 Ser Asp Ala Gln Met Asn Ile Ser Asp Asp Gly Thr Val Leu Ile Phe
 305 310 315 320
 Gln Asn Ala Gly Gly Ala Thr Pro Ser Thr Gly Val Thr Leu Cys Tyr
 325 330 335
 25 Asp Ser Gly Asn Val Ile Lys Asn Leu Ser Ser Thr Gly Ser Ala Asn
 340 345 350
 Leu Ser Ser Lys Asp Tyr Ala Thr Thr Lys Leu Arg Met Cys His Gly
 355 360 365
 Gln Ser Tyr Asn Asp Asn Asn Tyr Cys Asn Phe Thr Leu Ser Ile Asn
 370 375 380
 35 Thr Ile Glu Phe Thr Ser Tyr Gly Thr Phe Ser Ser Asp Gly Lys Gln
 385 390 395 400
 Phe Thr Pro Pro Ser Gly Ser Ala Ile Asp Leu His Leu Pro Asn Tyr
 405 410 415
 40 Val Asp Leu Asn Ala Leu Leu Asp Ile Ser Leu Asp Ser Leu Leu Asn
 420 425 430
 Tyr Asp Val Gln Gly Gln Phe Gly Gly Ser Asn Pro Val Asp Asn Phe
 435 440 445
 Ser Gly Pro Tyr Gly Ile Tyr Leu Trp Glu Ile Phe Phe His Ile Pro
 450 455 460
 50 Phe Leu Val Thr Val Arg Met Gln Thr Glu Gln Arg Tyr Glu Asp Ala
 465 470 475 480
 Asp Thr Trp Tyr Lys Tyr Ile Phe Arg Ser Ala Gly Tyr Arg Asp Ala
 485 490 495
 55 Asn Gly Gln Leu Ile Met Asp Gly Ser Lys Pro Arg Tyr Trp Asn Val
 500 505 510
 Met Pro Leu Gln Leu Asp Thr Ala Trp Asp Thr Thr Gln Pro Ala Thr
 515 520 525
 Thr Asp Pro Asp Val Ile Ala Met Ala Asp Pro Met His Tyr Lys Leu
 530 535 540
 65 Ala Ile Phe Leu His Thr Leu Asp Leu Leu Ile Ala Arg Gly Asp Ser
 545 550 555 560

Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Val Gln Ala Lys Met Tyr
565 570 575

5 Tyr Ile Gln Ala Gln Gln Leu Leu Gly Pro Arg Pro Asp Ile His Thr
580 585 590

Thr Asn Thr Trp Pro Asn Pro Thr Leu Ser Lys Glu Ala Gly Ala Ile
595 600 605

10 Ala Thr Pro Thr Phe Leu Ser Ser Pro Glu Val Met Thr Phe Ala Ala
610 615 620

15 Trp Leu Ser Ala Gly Asp Thr Ala Asn Ile Gly Asp Gly Asp Phe Leu
625 630 635 640

Pro Pro Tyr Asn Asp Val Leu Leu Gly Tyr Trp Asp Lys Leu Glu Leu
645 650 655

20 Arg Leu Tyr Asn Leu Arg His Asn Leu Ser Leu Asp Gly Gln Pro Leu
660 665 670

Asn Leu Pro Leu Tyr Ala Thr Pro Val Asp Pro Lys Thr Leu Gln Arg
675 680 685

25 Gln Gln Ala Gly Gly Asp Gly Thr Gly Ser Ser Pro Ala Gly Gly Gln
690 695 700

30 Gly Ser Val Gln Gly Trp Arg Tyr Pro Leu Leu Val Glu Arg Ala Arg
705 710 715 720

Ser Ala Val Ser Leu Leu Thr Gln Phe Gly Asn Ser Leu Gln Thr Thr
725 730 735

35 Leu Glu His Gln Asp Asn Glu Lys Met Thr Ile Leu Leu Gln Thr Gln
740 745 750

Gln Glu Ala Ile Leu Lys His Gln His Asp Ile Gln Gln Asn Asn Leu
755 760 765

40 Lys Gly Leu Gln His Ser Leu Thr Ala Leu Gln Ala Ser Arg Asp Gly
770 775 780

45 Asp Thr Leu Arg Gln Lys His Tyr Ser Asp Leu Ile Asn Gly Gly Leu
785 790 795 800

Ser Ala Ala Glu Ile Ala Gly Leu Thr Leu Arg Ser Thr Ala Met Ile
805 810 815

50 Thr Asn Gly Val Ala Thr Gly Leu Leu Ile Ala Gly Gly Ile Ala Asn
820 825 830

Ala Val Pro Asn Val Phe Gly Leu Ala Asn Gly Gly Ser Glu Trp Gly
835 840 845

55 Ala Pro Leu Ile Gly Ser Gly Gln Ala Thr Gln Val Gly Ala Gly Ile
850 855 860

60 Gln Asp Gln Ser Ala Gly Ile Ser Glu Val Thr Ala Gly Tyr Gln Arg
865 870 875 880

Arg Gln Glu Glu Trp Ala Leu Gln Arg Asp Ile Ala Asp Asn Glu Ile
885 890 895

65 Thr Gln Leu Asp Ala Gln Ile Gln Ser Leu Gln Glu Gln Ile Thr Met
900 905 910

(2) INFORMATION FOR SEQ ID NO:27:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1881 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

65 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- 5 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1881
 (D) OTHER INFORMATION: product = "P8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

10 ATG TCT GAA TCT TTA TTT ACA CAA ACG TTG AAA GAA GCG CGC CGT GAT 48
 Met Ser Glu Ser Leu Phe Thr Gln Thr Leu Lys Glu Ala Arg Arg Asp
 1 5 10 15

15 GCA TTG GTT GCT CAT TAT ATT GCT ACT CAG GTG CCC GCA GAT TTA AAA 96
 Ala Leu Val Ala His Tyr Ile Ala Thr Gln Val Pro Ala Asp Leu Lys
 20 25 30

20 GAG AGT ATC CAG ACC GCG GAT GAT CTG TAC GAA TAT CTG TTG CTG GAT 144
 Glu Ser Ile Gln Thr Ala Asp Asp Leu Tyr Glu Tyr Leu Leu Leu Asp
 35 40 45

25 ACC AAA ATT AGC GAT CTG GTT ACT ACT TCA CCG CTG TCC GAA GCG ATT 192
 Thr Lys Ile Ser Asp Leu Val Thr Thr Ser Pro Leu Ser Glu Ala Ile
 50 55 60

30 GGC AGT CTG CAA TTG TTT ATT CAT CGT GCG ATA GAG GGC TAT GAC GGC 240
 Gly Ser Leu Gln Leu Phe Ile His Arg Ala Ile Glu Gly Tyr Asp Gly
 65 70 75 80

35 ACG CTG GCA GAC TCA GCA AAA CCC TAT TTT GCC GAT GAA CAG TTT TTA 288
 Thr Leu Ala Asp Ser Ala Lys Pro Tyr Phe Ala Asp Glu Gln Phe Leu
 85 90 95

40 TAT AAC TGG GAT AGT TTT AAC CAC CGT TAT AGC ACT TGG GCT GGC AAG 336
 Tyr Asn Trp Asp Ser Phe Asn His Arg Tyr Ser Thr Trp Ala Gly Lys
 100 105 110

45 GAA CCG TTG AAA TTC TAT GCC GGG GAT TAT ATT GAT CCA ACA TTG CGA 384
 Glu Arg Leu Lys Phe Tyr Ala Gly Asp Tyr Ile Asp Pro Thr Leu Arg
 115 120 125

50 TTG AAT AAG ACC GAG ATA TTT ACC GCA TTT GAA CAA GGT ATT TCT CAA 432
 Leu Asn Lys Thr Glu Ile Phe Thr Ala Phe Glu Gln Gly Ile Ser Gln
 130 135 140

55 GGC AAA TTA AAA AGT GAA TTA GTC GAA TCT AAA TTA CGT GAT TAT CTA 480
 Gly Lys Leu Lys Ser Glu Leu Val Glu Ser Lys Leu Arg Asp Tyr Leu
 145 150 155 160

60 ATT AGT TAT GAC ACT TTA GCC ACC CTT GAT TAT ATT ACT GCC TGC CAA 528
 Ile Ser Tyr Asp Thr Leu Ala Thr Leu Asp Tyr Ile Thr Ala Cys Gln
 165 170 175

65 GGC AAA GAT AAT AAA ACC ATC TTC TTT ATT GGC CGT ACA CAG AAT GCA 576
 Gly Lys Asp Asn Lys Thr Ile Phe Phe Ile Gly Arg Thr Gln Asn Ala
 180 185 190

60 CCC TAT GCA TTT TAT TGG CGA AAA TTA ACT TTA GTC ACT GAT GGC GGT 624
 Pro Tyr Ala Phe Tyr Trp Arg Lys Leu Thr Leu Val Thr Asp Gly Gly
 195 200 205

65 AAG TTG AAA CCA GAT CAA TGG TCA GAG TGG CGA GCA ATT AAT GCC GCG 672
 Lys Leu Lys Pro Asp Gln Trp Ser Glu Trp Arg Ala Ile Asn Ala Gly
 210 215 220

ATT AGT GAG GCA TAT TCA GGG CAT CTC GAG CCT TTC TGG GAA AAT AAC 711
 Ile Ser Glu Ala Tyr Ser Gly His Val Glu Pro Phe Trp Glu Asn Asn 225 230 235 240
 5
 AAG CTG CAC ATC CGT TGG TTT ACT ATC TCG AAA GAA GAT AAA ATA GAT 758
 Lys Leu His Ile Arg Trp Phe Thr Ile Ser Lys Glu Asp Lys Ile Asp 245 250 255
 10
 TTT GTT TAT AAA AAC ATC TGG GTG ATG AGT AGC GAT TAT AGC TGG GCA 816
 Phe Val Tyr Lys Asn Ile Trp Val Met Ser Ser Asp Tyr Ser Trp Ala 260 265 270
 15
 TCA AAG AAA AAA ATC TTG GAA CTT TCT TTT ACT GAC TAC AAT AGA GTT 864
 Ser Lys Lys Lys Ile Leu Glu Leu Ser Phe Thr Asp Tyr Asn Arg Val 275 280 285
 20
 GGA GCA ACA GGA TCA TCA AGC CCG ACT GAA GTA GCT TCA CAA TAT GGT 912
 Gly Ala Thr Gly Ser Ser Ser Pro Thr Glu Val Ala Ser Gln Tyr Gly 290 295 300
 25
 TCT GAT GCT CAG ATG AAT ATT TCT GAT GAT GGG ACT GTA CTT ATT TTT 960
 Ser Asp Ala Gln Met Asn Ile Ser Asp Asp Gly Thr Val Leu Ile Phe 305 310 315 320
 CAG AAT GCC GGC GGA GCT ACT CCC AGT ACT GGA GTG ACG TTA TGT TAT 1008
 Gln Asn Ala Gly Gly Ala Thr Pro Ser Thr Gly Val Thr Leu Cys Tyr 325 330 335
 30
 GAC TCT GGC AAC GTG ATT AAG AAC CTA TCT AGT ACA GGA AGT GCA AAT 1056
 Asp Ser Gly Asn Val Ile Lys Asn Leu Ser Ser Thr Gly Ser Ala Asn 340 345 350
 35
 TTA TCG TCA AAG GAT TAT GCC ACA ACT AAA TTA CGC ATG TGT CAT GGA 1104
 Leu Ser Ser Lys Asp Tyr Ala Thr Thr Lys Leu Arg Met Cys His Gly 355 360 365
 40
 CAA AGT TAC AAT GAT AAT AAC TAC TGC AAT TTT ACA CTC TCT ATT AAT 1152
 Gln Ser Tyr Asn Asp Asn Asn Tyr Cys Asn Phe Thr Leu Ser Ile Asn 370 375 380
 45
 ACA ATA GAA TTC ACC TCC TAC GGC ACA TTC TCA TCA GAT GGA AAA CAA 1200
 Thr Ile Glu Phe Thr Ser Tyr Gly Thr Phe Ser Ser Asp Gly Lys Gln 385 390 395 400
 TTT ACA CCA CCT TCT GGT TCT GCC ATT GAT TTA CAC CTC CCT AAT TAT 1248
 Phe Thr Pro Pro Ser Gly Ser Ala Ile Asp Leu His Leu Pro Asn Tyr 405 410 415
 50
 GTA GAT CTC AAC GCG CTA TTA GAT ATT AGC CTC GAT TCA CTA CTT AAT 1296
 Val Asp Leu Asn Ala Leu Leu Asp Ile Ser Leu Asp Ser Leu Leu Asn 420 425 430
 55
 TAT GAC GTT CAG GGG CAG TTT GGC GGA TCT AAT CCG GTT GAT AAT TTC 1344
 Tyr Asp Val Gln Gly Gln Phe Gly Gly Ser Asn Pro Val Asp Asn Phe 435 440 445
 60
 AGT GGT CCC TAT GGT ATT TAT CTA TGG GAA ATC TTC TTC CAT ATT CCG 1392
 Ser Gly Pro Tyr Gly Ile Tyr Leu Trp Glu Ile Phe Phe His Ile Pro 450 455 460
 65
 TTC CTT GTT ACG GTC CGT ATG CAA ACC GAA CAA CGT TAC GAA GAC GCG 1440
 Phe Leu Val Thr Val Arg Met Gln Thr Glu Gln Arg Tyr Glu Asp Ala 465 470 475 480
 GAC ACT TGG TAC AAA TAT ATT TTC CGC AGC GCC GGT TAT CGC GAT GCT 1488

Asp Thr Trp Tyr Lys Tyr Ile Phe Arg Ser Ala Gly Tyr Arg Asp Ala
 485 490 495
 5 AAT GGC CAG CTC ATT ATG GAT GGC AGT AAA CCA CGT TAT TGG AAT GTG 1536
 Asn Gly Gln Leu Ile Met Asp Gly Ser Lys Pro Arg Tyr Trp Asn Val
 500 505 510
 10 ATG CCA TTG CAA CTG GAT ACC GCA TGG GAT ACC ACA CAG CCC GCC ACC 1534
 Met Pro Leu Gln Leu Asp Thr Ala Trp Asp Thr Thr Gln Pro Ala Thr
 515 520 525
 15 ACT GAT CCA GAT GTG ATC GCT ATG GCG GAC CCG ATG CAT TAC AAG CTC 1632
 Thr Asp Pro Asp Val Ile Ala Met Ala Asp Pro Met His Tyr Lys Leu
 530 535 540
 GCG ATA TTC CTG CAT ACC CTT GAT CTA TTG ATT GCC CGA GGC GAC AGC 1680
 Ala Ile Phe Leu His Thr Leu Asp Leu Leu Ile Ala Arg Gly Asp Ser
 545 550 555 560
 20 GCT TAC CGT CAA CTT GAA CGC GAT ACT CTA GTC GAA GCC AAA ATG TAC 1728
 Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Val Glu Ala Lys Met Tyr
 565 570 575
 25 TAC ATT CAG GCA CAA CAG CTA CTG GGA CCG CGC CCT GAT ATC CAT ACC 1776
 Tyr Ile Gln Ala Gln Gln Leu Leu Gly Pro Arg Pro Asp Ile His Thr
 580 585 590
 30 ACC AAT ACT TGG CCA AAT CCC ACC TTG AGT AAA GAA GCT GGC GCT ATT 1824
 Thr Asn Thr Trp Pro Asn Pro Thr Leu Ser Lys Glu Ala Gly Ala Ile
 595 600 605
 35 GCC ACA CCG ACA TTC CTC AGT TCA CCG GAG GTG ATG ACG TTC GCT GCC 1872
 Ala Thr Pro Thr Phe Leu Ser Ser Pro Glu Val Met Thr Phe Ala Ala
 610 615 620
 TGG CTA AGC 1881
 Trp Leu Ser
 625

40

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 627 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ser Glu Ser Leu Phe Thr Gln Thr Leu Lys Glu Ala Arg Arg Asp
 1 5 10 15
 55 Ala Leu Val Ala His Tyr Ile Ala Thr Gln Val Pro Ala Asp Leu Lys
 20 25 30
 60 Glu Ser Ile Gln Thr Ala Asp Asp Leu Tyr Glu Tyr Leu Leu Leu Asp
 35 40 45
 Thr Lys Ile Ser Asp Leu Val Thr Thr Ser Pro Leu Ser Glu Ala Ile
 50 55 60
 65 Gly Ser Leu Gln Leu Phe Ile His Arg Ala Ile Glu Gly Tyr Asp Gly

65 70 75 80
 Thr Leu Ala Asp Ser Ala Lys Pro Tyr Phe Ala Asp Glu Gln Phe Leu
 85 90 95
 5 Tyr Asn Trp Asp Ser Phe Asn His Arg Tyr Ser Thr Trp Ala Gly Lys
 100 105 110
 10 Glu Arg Leu Lys Phe Tyr Ala Gly Asp Tyr Ile Asp Pro Thr Leu Arg
 115 120 125
 Leu Asn Lys Thr Glu Ile Phe Thr Ala Phe Glu Gln Gly Ile Ser Gln
 130 135 140
 15 Gly Lys Leu Lys Ser Glu Leu Val Glu Ser Lys Leu Arg Asp Tyr Leu
 145 150 155 160
 Ile Ser Tyr Asp Thr Leu Ala Thr Leu Asp Tyr Ile Thr Ala Cys Gln
 165 170 175
 20 Gly Lys Asp Asn Lys Thr Ile Phe Phe Ile Gly Arg Thr Gln Asn Ala
 180 185 190
 25 Pro Tyr Ala Phe Tyr Trp Arg Lys Leu Thr Leu Val Thr Asp Gly Gly
 195 200 205
 Lys Leu Lys Pro Asp Gln Trp Ser Glu Trp Arg Ala Ile Asn Ala Gly
 210 215 220
 30 Ile Ser Glu Ala Tyr Ser Gly His Val Glu Pro Phe Trp Glu Asn Asn
 225 230 235 240
 Lys Leu His Ile Arg Trp Phe Thr Ile Ser Lys Glu Asp Lys Ile Asp
 245 250 255
 35 Phe Val Tyr Lys Asn Ile Trp Val Met Ser Ser Asp Tyr Ser Trp Ala
 260 265 270
 40 Ser Lys Lys Lys Ile Leu Glu Leu Ser Phe Thr Asp Tyr Asn Arg Val
 275 280 285
 Gly Ala Thr Gly Ser Ser Ser Pro Thr Glu Val Ala Ser Gln Tyr Gly
 290 295 300
 45 Ser Asp Ala Gln Met Asn Ile Ser Asp Asp Gly Thr Val Leu Ile Phe
 305 310 315 320
 Gln Asn Ala Gly Gly Ala Thr Pro Ser Thr Gly Val Thr Leu Cys Tyr
 325 330 335
 50 Asp Ser Gly Asn Val Ile Lys Asn Leu Ser Ser Thr Gly Ser Ala Asn
 340 345 350
 55 Leu Ser Ser Lys Asp Tyr Ala Thr Thr Lys Leu Arg Met Cys His Gly
 355 360 365
 Gln Ser Tyr Asn Asp Asn Asn Tyr Cys Asn Phe Thr Leu Ser Ile Asn
 370 375 380
 60 Thr Ile Glu Phe Thr Ser Tyr Gly Thr Phe Ser Ser Asp Gly Lys Gln
 385 390 395 400
 Phe Thr Pro Pro Ser Gly Ser Ala Ile Asp Leu His Leu Pro Asn Tyr
 405 410 415
 65 Val Asp Leu Asn Ala Leu Leu Asp Ile Ser Leu Asp Ser Leu Leu Asn

[illegible]

(2) INFORMATION FOR SEQ ID NO:29:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (genomic)

55 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1689
(D) OTHER INFORMATION: /product= "S8"

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCA GGC GAT ACC GCA AAT ATT GGC GAC GGT GAT TTC TTG CCA CCG TAC 48
Ala Gly Asp Thr Ala Asn Ile Gly Asp Gly Asp Phe Leu Pro Pro Tyr
1 5 10 15

	AAC GAT GTA CTA CTC GGT TAC TGG GAT AAA CTT GAG TTA CGC CTA TAC	35
	Asn Asp Val Leu Leu Gly Tyr Trp Asp Lys Leu Glu Leu Arg Leu Tyr	
	20 25 30	
5	AAC CTG CGC CAC AAT CTG AGT CTG GAT GGT CAA CCG CTA AAT CTG CCA	144
	Asn Leu Arg His Asn Leu Ser Leu Asp Gly Gln Pro Leu Asn Leu Pro	
	35 40 45	
10	CTG TAT GCC ACG CCG GTA GAC CCG AAA ACC CTG CAA CGC CAG CAA GCC	132
	Leu Tyr Ala Thr Pro Val Asp Pro Lys Thr Leu Gln Arg Gln Gln Ala	
	50 55 60	
15	GGA GGG GAC GGT ACA GGC AGT AGT CCG GCT GGT GGT CAA GGC AGT GTT	240
	Gly Gly Asp Gly Thr Gly Ser Ser Pro Ala Gly Gly Gln Gly Ser Val	
	65 70 75 80	
20	CAG GGC TGG CGC TAT CCG TTA TTG GTA GAA CGC GCC CGC TCT GCC GTG	288
	Gln Gly Trp Arg Tyr Pro Leu Leu Val Glu Arg Ala Arg Ser Ala Val	
	85 90 95	
25	AGT TTG TTG ACT CAG TTC GGC AAC AGC TTA CAA ACA ACG TTA GAA CAT	336
	Ser Leu Leu Thr Gln Phe Gly Asn Ser Leu Gln Thr Thr Leu Glu His	
	100 105 110	
30	CAG GAT AAT GAA AAA ATG ACG ATA CTG TTG CAG ACT CAA CAG GAA GCC	384
	Gln Asp Asn Glu Lys Met Thr Ile Leu Leu Gln Thr Gln Gln Glu Ala	
	115 120 125	
35	ATC CTG AAA CAT CAG CAC GAT ATA CAA CAA AAT AAT CTA AAA GGA TTA	432
	Ile Leu Lys His Gln His Asp Ile Gln Gln Asn Asn Leu Lys Gly Leu	
	130 135 140	
40	CAA CAC AGC CTG ACC GCA TTA CAG GCT AGC CGT GAT GGC GAC ACA TTG	480
	Gln His Ser Leu Thr Ala Leu Gln Ala Ser Arg Asp Gly Asp Thr Leu	
	145 150 155 160	
45	CGG CAA AAA CAT TAC AGC GAC CTG ATT AAC GGT GGT CTA TCT GCG GCA	528
	Arg Gln Lys His Tyr Ser Asp Leu Ile Asn Gly Gly Leu Ser Ala Ala	
	165 170 175	
50	GAA ATC GCC GGT CTG ACA CTA CGC AGC ACC GCC ATG ATT ACC AAT GGC	576
	Glu Ile Ala Gly Leu Thr Leu Arg Ser Thr Ala Met Ile Thr Asn Gly	
	180 185 190	
55	GTT GCA ACG GGA TTG CTG ATT GCC GGC GGA ATC GCC AAC GCG GTA CCT	624
	Val Ala Thr Gly Leu Leu Ile Ala Gly Gly Ile Ala Asn Ala Val Pro	
	195 200 205	
60	AAC GTC TTC GGG CTG GCT AAC GGT GGA TCG GAA TGG GGA GCG CCA TTA	672
	Asn Val Phe Gly Leu Ala Asn Gly Gly Ser Glu Trp Gly Ala Pro Leu	
	210 215 220	
65	ATT GGC TCC GGG CAA GCA ACC CAA GTT GGC GCC GGC ATC CAG GAT CAG	720
	Ile Gly Ser Gly Gln Ala Thr Gln Val Gly Ala Gly Ile Gln Asp Gln	
	225 230 235 240	
70	AGC GCG GGC ATT TCA GAA GTG ACA GCA GGC TAT CAG CGT CGT CAG GAA	768
	Ser Ala Gly Ile Ser Glu Val Thr Ala Gly Tyr Gln Arg Arg Gln Glu	
	245 250 255	
75	GAA TGG GCA TTG CAA CGG GAT ATT GCT GAT AAC GAA ATA ACC CAA CTG	816
	Glu Trp Ala Leu Gln Arg Asp Ile Ala Asp Asn Glu Ile Thr Gln Leu	
	260 265 270	
80	GAT GCC CAG ATA CAA AGC CTG CAA GAG CAA ATC ACG ATG GCA CAA AAA	864

Asp Ala Gln Ile Gln Ser Leu Gln Glu Gln Ile Thr Met Ala Gln Lys
 275 280 285
 5 CAG ATC ACG CTC TCT GAA ACC GAA CAA GCG AAT GCC CAA GCG ATT TAT 292
 Gln Ile Thr Leu Ser Glu Thr Glu Gln Ala Asn Ala Gln Ala Ile Tyr
 290 295 300
 10 GAC CTG CAA ACC ACT CGT TTT ACC GGG CAG GCA CTG TAT AAC TGG ATG 296
 Asp Leu Gln Thr Thr Arg Phe Thr Gly Gln Ala Leu Tyr Asn Trp Met
 305 310 315 320
 15 GCC GGT CGT CTC TCC GCG CTC TAT TAC CAA ATG TAT GAT TCC ACT CTG 1008
 Ala Gly Arg Leu Ser Ala Leu Tyr Tyr Gln Met Tyr Asp Ser Thr Leu
 325 330 335
 20 CCA ATC TGT CTC CAG CCA AAA GCC GCA TTA GTA CAG GAA TTA GGC GAG 1056
 Pro Ile Cys Leu Gln Pro Lys Ala Ala Leu Val Gln Glu Leu Gly Glu
 340 345 350
 25 AAA GAG AGC GAC AGT CTT TTC CAG GTT CCG GTG TGG AAT GAT CTG TCG 1104
 Lys Glu Ser Asp Ser Leu Phe Gln Val Pro Val Trp Asn Asp Leu Trp
 355 360 365
 30 CAA GGG CTG TTA GCA GGA GAA GGT TTA AGT TCA GAG CTA CAG AAA CTG 1152
 Gln Gly Leu Leu Ala Gly Glu Gly Leu Ser Ser Glu Leu Gln Lys Leu
 370 375 380
 35 GAT GCC ATC TGG CTT GCA CGT GGT GGT ATT GGG CTA GAA GCC ATC CGC 1200
 Asp Ala Ile Trp Leu Ala Arg Gly Gly Ile Gly Leu Glu Ala Ile Arg
 385 390 395 400
 40 ACC GTG TCG CTG GAT ACC CTG TTT GGC ACA GGG ACG TTA AGT GAA AAT 1248
 Thr Val Ser Leu Asp Thr Leu Phe Gly Thr Gly Thr Leu Ser Glu Asn
 405 410 415
 45 ATC AAT AAA GTG CTT AAC GGG GAA ACG GTA TCT CCA TCC GGT GGC GTC 1296
 Ile Asn Lys Val Leu Asn Gly Glu Thr Val Ser Pro Ser Gly Gly Val
 420 425 430
 50 ACT CTG GCG CTG ACA GGG GAT ATC TTC CAA GCA ACA CTG GAT TTG AGT 1344
 Thr Leu Ala Leu Thr Gly Asp Ile Phe Gln Ala Thr Leu Asp Leu Ser
 435 440 445
 55 CAG CTA GGT TTG GAT AAC TCT TAC AAC TTG GGT AAC GAG AAG AAA CGT 1392
 Gln Leu Gly Leu Asp Asn Ser Tyr Asn Leu Gly Asn Glu Lys Lys Arg
 450 455 460
 60 CGT ATT AAA CGT ATC GCC GTC ACC CTG CCA ACA CTT CTG GGG CCA TAT 1440
 Arg Ile Lys Arg Ile Ala Val Thr Leu Pro Thr Leu Leu Gly Pro Tyr
 465 470 475 480
 65 CAA GAT CTT GAA GCC ACA CTG GTA ATG GGT GCG GAA ATC GCC GCC TTA 1488
 Gln Asp Leu Glu Ala Thr Leu Val Met Gly Ala Glu Ile Ala Ala Leu
 485 490 495
 70 TCA CAC GGT GTG AAT GAC GGA GGC CGG TTT GTT ACC GAC TTT AAC GAC 1536
 Ser His Gly Val Asn Asp Gly Gly Arg Phe Val Thr Asp Phe Asn Asp
 500 505 510
 75 AGC CGT TTT CTG CCT TTT GAA GGT CGA GAT GCA ACA ACC GGC ACA CTG 1584
 Ser Arg Phe Leu Pro Phe Glu Gly Arg Asp Ala Thr Thr Gly Thr Leu
 515 520 525
 80 GAG CTC AAT ATT TTC CAT GCG GGT AAA GAG GGA ACG CAA CAC GAG TTG 1632
 Glu Leu Asn Ile Phe His Ala Gly Lys Glu Gly Thr Gln His Glu Leu
 530 535 540

CTC GCG AAT CTG AGT GAC ATC ATT GTG CAT CTG AAT TAC ATC ATT CGA 1550
 Val Ala Asn Leu Ser Asp Ile Ile Val His Leu Asn Tyr Ile Ile Arg
 545 550 555 560

GAC GCG TAA
 Asp Ala *

1559

10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 563 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ala Gly Asp Thr Ala Asn Ile Gly Asp Gly Asp Phe Leu Pro Pro Tyr
 1 5 10 15
 Asn Asp Val Leu Leu Gly Tyr Trp Asp Lys Leu Glu Leu Arg Leu Tyr
 20 25 30
 Asn Leu Arg His Asn Leu Ser Leu Asp Gly Gln Pro Leu Asn Leu Pro
 35 40 45
 Leu Tyr Ala Thr Pro Val Asp Pro Lys Thr Leu Gln Arg Gln Gln Ala
 50 55 60
 Gly Gly Asp Gly Thr Gly Ser Ser Pro Ala Gly Gly Gln Gly Ser Val
 65 70 75 80
 Gln Gly Trp Arg Tyr Pro Leu Leu Val Glu Arg Ala Arg Ser Ala Val
 85 90 95
 Ser Leu Leu Thr Gln Phe Gly Asn Ser Leu Gln Thr Thr Leu Glu His
 100 105 110
 Gln Asp Asn Glu Lys Met Thr Ile Leu Leu Gln Thr Gln Gln Glu Ala
 115 120 125
 Ile Leu Lys His Gln His Asp Ile Gln Gln Asn Asn Leu Lys Gly Leu
 130 135 140
 Gln His Ser Leu Thr Ala Leu Gln Ala Ser Arg Asp Gly Asp Thr Leu
 145 150 155 160
 Arg Gln Lys His Tyr Ser Asp Leu Ile Asn Gly Gly Leu Ser Ala Ala
 165 170 175
 Glu Ile Ala Gly Leu Thr Leu Arg Ser Thr Ala Met Ile Thr Asn Gly
 180 185 190
 Val Ala Thr Gly Leu Leu Ile Ala Gly Gly Ile Ala Asn Ala Val Pro
 195 200 205
 Asn Val Phe Gly Leu Ala Asn Gly Gly Ser Glu Trp Gly Ala Pro Leu
 210 215 220
 Ile Gly Ser Gly Gln Ala Thr Gln Val Gly Ala Gly Ile Gln Asp Gln

225 230 235 240
 Ser Ala Gly Ile Ser Glu Val Thr Ala Gly Tyr Gln Arg Arg Gln Glu
 245 250 255
 5 Glu Trp Ala Leu Gln Arg Asp Ile Ala Asp Asn Glu Ile Thr Gln Leu
 260 265 270
 10 Asp Ala Gln Ile Gln Ser Leu Gln Glu Gln Ile Thr Met Ala Gln Lys
 275 280 285
 Gln Ile Thr Leu Ser Glu Thr Glu Gln Ala Asn Ala Gln Ala Ile Tyr
 290 295 300
 15 Asp Leu Gln Thr Thr Arg Phe Thr Gly Gln Ala Leu Tyr Asn Trp Met
 305 310 315 320
 Ala Gly Arg Leu Ser Ala Leu Tyr Tyr Gln Met Tyr Asp Ser Thr Leu
 325 330 335
 20 Pro Ile Cys Leu Gln Pro Lys Ala Ala Leu Val Gln Glu Leu Gly Glu
 340 345 350
 25 Lys Glu Ser Asp Ser Leu Phe Gln Val Pro Val Trp Asn Asp Leu Trp
 355 360 365
 Gln Gly Leu Leu Ala Gly Glu Gly Leu Ser Ser Glu Leu Gln Lys Leu
 370 375 380
 30 Asp Ala Ile Trp Leu Ala Arg Gly Gly Ile Gly Leu Glu Ala Ile Arg
 385 390 395 400
 Thr Val Ser Leu Asp Thr Leu Phe Gly Thr Gly Thr Leu Ser Glu Asn
 405 410 415
 35 Ile Asn Lys Val Leu Asn Gly Glu Thr Val Ser Pro Ser Gly Gly Val
 420 425 430
 40 Thr Leu Ala Leu Thr Gly Asp Ile Phe Gln Ala Thr Leu Asp Leu Ser
 435 440 445
 Gln Leu Gly Leu Asp Asn Ser Tyr Asn Leu Gly Asn Glu Lys Lys Arg
 450 455 460
 45 Arg Ile Lys Arg Ile Ala Val Thr Leu Pro Thr Leu Leu Gly Pro Tyr
 465 470 475 480
 Gln Asp Leu Glu Ala Thr Leu Val Met Gly Ala Glu Ile Ala Ala Leu
 485 490 495
 50 Ser His Gly Val Asn Asp Gly Gly Arg Phe Val Thr Asp Phe Asn Asp
 500 505 510
 55 Ser Arg Phe Leu Pro Phe Glu Gly Arg Asp Ala Thr Thr Gly Thr Leu
 515 520 525
 Glu Leu Asn Ile Phe His Ala Gly Lys Glu Gly Thr Gln His Glu Leu
 530 535 540
 60 Val Ala Asn Leu Ser Asp Ile Ile Val His Leu Asn Tyr Ile Ile Arg
 545 550 555 560
 Asp Ala •

65

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 4458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- 15 (A) NAME/KEY: CDS
 (B) LOCATION: 1..4458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

20 ATG CAG GAT TCA CCA GAA GTA TCG ATT ACA ACG CTG TCA CTT CCC AAA 48
 Met Gln Asp Ser Pro Glu Val Ser Ile Thr Thr Leu Ser Leu Pro Lys
 1 5 10 15

25 GGT GGC GGT GCT ATC AAT GGC ATG GGA GAA GCA CTG AAT GCT GCC GGC 96
 Gly Gly Gly Ala Ile Asn Gly Met Gly Glu Ala Leu Asn Ala Ala Gly
 20 25 30

30 CCT GAT GGA ATG GCC TCC CTA TCT CTG CCA TTA CCC CTT TCG ACC GGC 144
 Pro Asp Gly Met Ala Ser Leu Ser Leu Pro Leu Pro Leu Ser Thr Gly
 35 40 45

35 AGA GGG ACG GCT CCT GGA TTA TCG CTG ATT TAC AGC AAC AGT GCA GGT 192
 Arg Gly Thr Ala Pro Gly Leu Ser Leu Ile Tyr Ser Asn Ser Ala Gly
 50 55 60

40 AAT GGG CCT TTC GGC ATC GGC TGG CAA TGC GGT GTT ATG TCC ATT AGC 240
 Asn Gly Pro Phe Gly Ile Gly Trp Gln Cys Gly Val Met Ser Ile Ser
 65 70 75 80

45 CGA CGC ACC CAA CAT GGC ATT CCA CAA TAC GGT AAT GAC GAC ACG TTC 288
 Arg Arg Thr Gln His Gly Ile Pro Gln Tyr Gly Asn Asp Asp Thr Phe
 85 90 95

50 CTA TCC CCA CAA GGC GAG GTC ATG AAT ATC GCC CTG AAT GAC CAA GGC 336
 Leu Ser Pro Gln Gly Glu Val Met Asn Ile Ala Leu Asn Asp Gln Gly
 100 105 110

55 CAA CCT GAT ATC CGT CAA GAC GTT AAA ACG CTG CAA GGC GTT ACC TTG 384
 Gln Pro Asp Ile Arg Gln Asp Val Lys Thr Leu Gln Gly Val Thr Leu
 115 120 125

60 CCA ATT TCC TAT ACC GTG ACC CGC TAT CAA GCC CGC CAG ATC CTG GAT 432
 Pro Ile Ser Tyr Thr Val Thr Arg Tyr Gln Ala Arg Gln Ile Leu Asp
 130 135 140

55 TTC AGT AAA ATC GAA TAC TGG CAA CCT GCC TCC GGT CAA GAA GGA CGC 480
 Phe Ser Lys Ile Glu Tyr Trp Gln Pro Ala Ser Gly Gln Glu Gly Arg
 145 150 155 160

60 GCT TTC TGG CTG ATA TCG ACA CCG GAC GGC CAT CTA CAC ATC TTA GGC 528
 Ala Phe Trp Leu Ile Ser Thr Pro Asp Gly His Leu His Ile Leu Gly
 165 170 175

AAA ACC GCG CAG GCT TGT CTG GCA AAT CCG CAA AAT GAC CAA CAA ATC 576
 Lys Thr Ala Gln Ala Cys Leu Ala Asn Pro Gln Asn Asp Gln Gln Ile

180 135 190
 5 GCC CAG TGG TTG CTG GAA GAA ACT GTG ACG CCA GCC GGT GAA CAT GTC 624
 Ala Gln Trp Leu Leu Glu Glu Thr Val Thr Pro Ala Gly Glu His Val
 195 200 205
 10 AGC TAT CAA TAT CGA GCC GAA GAT GAA GCC CAT TGT GAC GAC AAT GAA 672
 Ser Tyr Gln Tyr Arg Ala Glu Asp Glu Ala His Cys Asp Asp Asn Glu
 210 215 220
 AAA ACC GCT CAT CCC AAT GTT ACC GCA CAG CGC TAT CTG GTA CAG GTG 720
 Lys Thr Ala His Pro Asn Val Thr Ala Gln Arg Tyr Leu Val Gln Val
 225 230 235 240
 15 AAC TAC GGC AAC ATC AAA CCA CAA GCC AGC CTG TTC GTA CTG GAT AAC 758
 Asn Tyr Gly Asn Ile Lys Pro Gln Ala Ser Leu Phe Val Leu Asp Asn
 245 250 255
 20 GCA CCT CCC GCA CCG GAA GAG TGG CTG TTT CAT CTG GTC TTT GAC CAC 816
 Ala Pro Pro Ala Pro Glu Glu Trp Leu Phe His Leu Val Phe Asp His
 260 265 270
 25 GGT GAG CGC GAT ACC TCA CTT CAT ACC GTG CCA ACA TGG GAT GCA GGT 864
 Gly Glu Arg Asp Thr Ser Leu His Thr Val Pro Thr Trp Asp Ala Gly
 275 280 285
 30 ACA GCG CAA TGG TCT GTA CGC CCG GAT ATC TTC TCT CGC TAT GAA TAT 912
 Thr Ala Gln Trp Ser Val Arg Pro Asp Ile Phe Ser Arg Tyr Glu Tyr
 290 295 300
 GGT TTT GAA GTG CGT ACT CGC CGC TTA TGT CAA CAA GTG CTG ATG TTT 960
 Gly Phe Glu Val Arg Thr Arg Arg Leu Cys Gln Gln Val Leu Met Phe
 305 310 315 320
 35 CAC CGC ACC GCG CTC ATG GCC GGA GAA GCC AGT ACC AAT GAC GCC CCG 1008
 His Arg Thr Ala Leu Met Ala Gly Glu Ala Ser Thr Asn Asp Ala Pro
 325 330 335
 40 GAA CTG GTT GGA CGC TTA ATA CTG GAA TAT GAC AAA AAC GCC AGC GTC 1056
 Glu Leu Val Gly Arg Leu Ile Leu Glu Tyr Asp Lys Asn Ala Ser Val
 340 345 350
 45 ACC ACG TTG ATT ACC ATC CGT CAA TTA AGC CAT GAA TCG GAC GGG AGG 1104
 Thr Thr Leu Ile Thr Ile Arg Gln Leu Ser His Glu Ser Asp Gly Arg
 355 360 365
 50 CCA GTC ACC CAG CCA CCA CTA GAA CTA GCC TGG CAA CGG TTT GAT CTG 1152
 Pro Val Thr Gln Pro Pro Leu Glu Leu Ala Trp Gln Arg Phe Asp Leu
 370 375 380
 GAG AAA ATC CCG ACA TGG CAA CGC TTT GAC GCA CTA GAT AAT TTT AAC 1200
 Glu Lys Ile Pro Thr Trp Gln Arg Phe Asp Ala Leu Asp Asn Phe Asn
 385 390 395 400
 55 TCG CAG CAA CGT TAT CAA CTG GTT GAT CTG CGG GGA GAA GGG TTG CCA 1248
 Ser Gln Gln Arg Tyr Gln Leu Val Asp Leu Arg Gly Glu Gly Leu Pro
 405 410 415
 60 GGT ATG CTG TAT CAA GAT CGA GGC GCT TGG TGG TAT AAA GCT CCG CAA 1296
 Gly Met Leu Tyr Gln Asp Arg Gly Ala Trp Trp Tyr Lys Ala Pro Gln
 420 425 430
 65 CGT CAG GAA GAC GGA GAC AGC AAT GCC GTC ACT TAC GAC AAA ATC GCC 1344
 Arg Gln Glu Asp Gly Asp Ser Asn Ala Val Thr Tyr Asp Lys Ile Ala
 435 440 445

	TTA	TTG	GCT	ACC	CTA	CCC	AAT	TTG	CAG	GAT	AAT	GCC	TCA	TTG	ATG	GAT	1391
	Pro	Leu	Pro	Thr	Leu	Pro	Asn	Leu	Gln	Asp	Asn	Ala	Ser	Leu	Met	Asp	
	450						455					460					
5	ATC	AAC	GGA	GAC	GGC	CAA	CTG	GAT	TGG	GTT	GTT	ACC	GCC	TCC	GGT	ATT	1445
	Ile	Asn	Gly	Asp	Gly	Gln	Leu	Asp	Trp	Val	Val	Thr	Ala	Ser	Gly	Ile	
	465					470					475					480	
10	CGC	GGA	TAC	CAT	AGT	CAG	CAA	CCC	GAT	GGA	AAG	TGG	ACG	CAC	TTT	ACG	1438
	Arg	Gly	Tyr	His	Ser	Gln	Gln	Pro	Asp	Gly	Lys	Trp	Thr	His	Phe	Thr	
					485					490						495	
15	CCA	ATC	AAT	GCC	TTG	CCC	GTG	GAA	TAT	TTT	CAT	CCA	AGC	ATC	CAG	TTC	1536
	Pro	Ile	Asn	Ala	Leu	Pro	Val	Glu	Tyr	Phe	His	Pro	Ser	Ile	Gln	Phe	
				500					505						510		
20	GCT	GAC	CTT	ACC	GGG	GCA	GGC	TTA	TCT	GAT	TTA	GTG	TTG	ATC	GGG	CCG	1584
	Ala	Asp	Leu	Thr	Gly	Ala	Gly	Leu	Ser	Asp	Leu	Val	Leu	Ile	Gly	Pro	
			515					520					525				
25	AAA	AGC	GTG	CGT	CTA	TAT	GCC	AAC	CAG	CGA	AAC	GGC	TGG	CGT	AAA	GGA	1632
	Lys	Ser	Val	Arg	Leu	Tyr	Ala	Asn	Gln	Arg	Asn	Gly	Trp	Arg	Lys	Gly	
		530					535					540					
30	GAA	GAT	GTC	CCC	CAA	TCC	ACA	GGT	ATC	ACC	CTG	CCT	GTC	ACA	GGG	ACC	1680
	Glu	Asp	Val	Pro	Gln	Ser	Thr	Gly	Ile	Thr	Leu	Pro	Val	Thr	Gly	Thr	
	545					550					555					560	
35	GAT	GCC	CGC	AAA	CTG	GTG	GCT	TTC	AGT	GAT	ATG	CTC	GGT	TCC	GGT	CAA	1728
	Asp	Ala	Arg	Lys	Leu	Val	Ala	Phe	Ser	Asp	Met	Leu	Gly	Ser	Gly	Gln	
					565					570					575		
40	CAA	CAT	CTG	GTG	GAA	ATC	AAG	GGT	AAT	CGC	GTC	ACC	TGT	TGG	CCG	AAT	1776
	Gln	His	Leu	Val	Glu	Ile	Lys	Gly	Asn	Arg	Val	Thr	Cys	Trp	Pro	Asn	
				580				585						590			
45	CTA	GGG	CAT	GGC	CGT	TTC	GGT	CAA	CCA	CTA	ACT	CTG	TCA	GGA	TTT	AGC	1824
	Leu	Gly	His	Gly	Arg	Phe	Gly	Gln	Pro	Leu	Thr	Leu	Ser	Gly	Phe	Ser	
			595					600					605				
50	CAG	CCC	GAA	AAT	AGC	TTC	AAT	CCC	GAA	CGG	CTG	TTT	CTG	GCG	GAT	ATC	1872
	Gln	Pro	Glu	Asn	Ser	Phe	Asn	Pro	Glu	Arg	Leu	Phe	Leu	Ala	Asp	Ile	
		610					615					620					
55	GAC	GGC	TCC	GGC	ACC	ACC	GAC	CTT	ATC	TAT	GCG	CAA	TCC	GGC	TCT	TTG	1920
	Asp	Gly	Ser	Gly	Thr	Thr	Asp	Leu	Ile	Tyr	Ala	Gln	Ser	Gly	Ser	Leu	
	625					630					635					640	
60	CTC	ATT	TAT	CTC	AAC	CAA	AGT	GGT	AAT	CAG	TTT	GAT	GCC	CCG	TTG	ACA	1968
	Leu	Ile	Tyr	Leu	Asn	Gln	Ser	Gly	Asn	Gln	Phe	Asp	Ala	Pro	Leu	Thr	
					645					650					655		
65	TTA	GCG	TTG	CCA	GAA	GGC	GTA	CAA	TTT	GAC	AAC	ACT	TGC	CAA	CTT	CAA	2016
	Leu	Ala	Leu	Pro	Glu	Gly	Val	Gln	Phe	Asp	Asn	Thr	Cys	Gln	Leu	Gln	
				660					665					670			
70	GTC	GCC	GAT	ATT	CAG	GGA	TTA	GGG	ATA	GCC	AGC	TTG	ATT	CTG	ACT	GTG	2064
	Val	Ala	Asp	Ile	Gln	Gly	Leu	Gly	Ile	Ala	Ser	Leu	Ile	Leu	Thr	Val	
			675					680					685				
75	CCA	CAT	ATC	GCG	CCA	CAT	CAC	TGG	CGT	TGT	GAC	CTG	TCA	CTG	ACC	AAA	2112
	Pro	His	Ile	Ala	Pro	His	His	Trp	Arg	Cys	Asp	Leu	Ser	Leu	Thr	Lys	
			690				695					700					
80	CCC	TGG	TTG	TTG	AAT	GTA	ATG	AAC	AAT	AAC	CGG	GGC	GCA	CAT	CAC	ACG	2160
	Pro	Trp	Leu	Leu	Asn	Val	Met	Asn	Asn	Asn	Arg	Gly	Ala	His	His	Thr	

	705	710	715	720	
5	CTA CAT TAT CGT AGT TCC GCG CAA TTC TGG TTG GAT GAA AAA TTA CAG 2203 Leu His Tyr Arg Ser Ser Ala Gln Phe Trp Leu Asp Glu Lys Leu Gln 725 730 735				
10	CTC ACC AAA GCA GGC AAA TCT CCG GCT TGT TAT CTG CCG TTT CCA ATG 2256 Leu Thr Lys Ala Gly Lys Ser Pro Ala Cys Tyr Leu Pro Phe Pro Met 740 745 750				
15	CAT TTG CTA TGG TAT ACC GAA ATT CAG GAT GAA ATC AGC GGC AAC CCG 2304 His Leu Leu Trp Tyr Thr Glu Ile Gln Asp Glu Ile Ser Gly Asn Arg 755 760 765				
20	CTC ACC AGT GAA GTC AAC TAC AGC CAC GGC GTC TGG GAT GGT AAA GAG 2352 Leu Thr Ser Glu Val Asn Tyr Ser His Gly Val Trp Asp Gly Lys Glu 770 775 780				
25	CGG GAA TTC AGA GGA TTT GGC TGC ATC AAA CAG ACA GAT ACC ACA ACG 2400 Arg Glu Phe Arg Gly Phe Gly Cys Ile Lys Gln Thr Asp Thr Thr Thr 785 790 795 800				
30	TTT TCT CAC GGC ACC GCC CCC GAA CAG GCG GCA CCG TCG CTG AGT ATT 2448 Phe Ser His Gly Thr Ala Pro Glu Gln Ala Ala Pro Ser Leu Ser Ile 805 810 815				
35	AGC TGG TTT GCC ACC GGC ATG GAT GAA GTA GAC AGC CAA TTA GCT ACG 2496 Ser Trp Phe Ala Thr Gly Met Asp Glu Val Asp Ser Gln Leu Ala Thr 820 825 830				
40	GAA TAT TGG CAG GCA GAC ACG CAA GCT TAT AGC GGA TTT GAA ACC CGT 2544 Glu Tyr Trp Gln Ala Asp Thr Gln Ala Tyr Ser Gly Phe Glu Thr Arg 835 840 845				
45	TAT ACC GTC TGG GAT CAC ACC AAC CAG ACA GAC CAA GCA TTT ACC CCC 2592 Tyr Thr Val Trp Asp His Thr Asn Gln Thr Asp Gln Ala Phe Thr Pro 850 855 860				
50	AAT GAG ACA CAA CGT AAC TGG CTG ACG CGA GCG CTT AAA GGC CAA CTG 2640 Asn Glu Thr Gln Arg Asn Trp Leu Thr Arg Ala Leu Lys Gly Gln Leu 865 870 875 880				
55	CTA CGC ACT GAG CTC TAC GGT CTG GAC GGA ACA GAT AAG CAA ACA GTG 2688 Leu Arg Thr Glu Leu Tyr Gly Leu Asp Gly Thr Asp Lys Gln Thr Val 885 890 895				
60	CCT TAT ACC GTC AGT GAA TCG CGC TAT CAG GTA CGC TCT ATT CCC GTA 2736 Pro Tyr Thr Val Ser Glu Ser Arg Tyr Gln Val Arg Ser Ile Pro Val 900 905 910				
65	AAT AAA GAA ACT GAA TTA TCT GCC TCG GTG ACT GCT ATT GAA AAT CGC 2784 Asn Lys Glu Thr Glu Leu Ser Ala Trp Val Thr Ala Ile Glu Asn Arg 915 920 925				
70	AGC TAC CAC TAT GAA CGT ATC ATC ACT GAC CCA CAG TTC AGC CAG AGT 2832 Ser Tyr His Tyr Glu Arg Ile Ile Thr Asp Pro Gln Phe Ser Gln Ser 930 935 940				
75	ATC AAG TTG CAA CAC GAT ATC TTT GGT CAA TCA CTG CAA AGT GTC GAT 2880 Ile Lys Leu Gln His Asp Ile Phe Gly Gln Ser Leu Gln Ser Val Asp 945 950 955 960				
80	ATT GCC TGG CCG CGC CGC GAA AAA CCA GCA GTG AAT CCC TAC CCG CCT 2928 Ile Ala Trp Pro Arg Arg Glu Lys Pro Ala Val Asn Pro Tyr Pro Pro 965 970 975				

	ACT	CTG	CCG	GAA	ACG	CTA	TTT	GAC	AGC	AGC	TAT	GAT	GAT	CAA	CAA	CAA	3976
	Thr	Leu	Pro	Glu	Thr	Leu	Phe	Asp	Ser	Ser	Tyr	Asp	Asp	Gln	Gln	Gln	
				980					985					990			
5	CTA	TTA	CGT	CTG	GTG	AGA	CAA	AAA	AAT	AGC	TGG	CAT	CAC	CTG	ACT	GAT	3024
	Leu	Leu	Arg	Leu	Val	Arg	Gln	Lys	Asn	Ser	Trp	His	His	Leu	Thr	Asp	
			995					1000					1005				
10	GGG	GAA	AAC	TGG	CGA	TTA	GGT	TTA	CCG	AAT	GCA	CAA	CGC	CGT	GAT	GTT	3072
	Gly	Glu	Asn	Trp	Arg	Leu	Gly	Leu	Pro	Asn	Ala	Gln	Arg	Arg	Asp	Val	
		1010					1015					1020					
15	TAT	ACT	TAT	GAC	CGG	AGC	AAA	ATT	CCA	ACC	GAA	GGG	ATT	TCC	CTT	GAA	3120
	Tyr	Thr	Tyr	Asp	Arg	Ser	Lys	Ile	Pro	Thr	Glu	Gly	Ile	Ser	Leu	Glu	
	1025					1030					1035				1040		
20	ATC	TTG	CTG	AAA	GAT	GAT	GGC	CTG	CTA	GCA	GAT	GAA	AAA	GCG	GCC	GTT	3168
	Ile	Leu	Leu	Lys	Asp	Asp	Gly	Leu	Leu	Ala	Asp	Glu	Lys	Ala	Ala	Val	
				1045						1050				1055			
	TAT	CTG	GGA	CAA	CAA	CAG	ACG	TTT	TAC	ACC	GCC	GGT	CAA	GCG	GAA	GTC	3216
	Tyr	Leu	Gly	Gln	Gln	Gln	Thr	Phe	Tyr	Thr	Ala	Gly	Gln	Ala	Glu	Val	
				1060					1065					1070			
25	ACT	CTA	GAA	AAA	CCC	ACG	TTA	CAA	GCA	CTG	GTC	GCG	TTC	CAA	GAA	ACC	3264
	Thr	Leu	Glu	Lys	Pro	Thr	Leu	Gln	Ala	Leu	Val	Ala	Phe	Gln	Glu	Thr	
			1075					1080					1085				
30	GCC	ATG	ATG	GAC	GAT	ACC	TCA	TTA	CAG	GCG	TAT	GAA	GGC	GTG	ATT	GAA	3312
	Ala	Met	Met	Asp	Asp	Thr	Ser	Leu	Gln	Ala	Tyr	Glu	Gly	Val	Ile	Glu	
		1090					1095					1100					
35	GAG	CAA	GAG	TTG	AAT	ACC	GCG	CTG	ACA	CAG	GCC	GGT	TAT	CAG	CAA	GTC	3360
	Glu	Gln	Glu	Leu	Asn	Thr	Ala	Leu	Thr	Gln	Ala	Gly	Tyr	Gln	Gln	Val	
	1105				1110					1115				1120			
40	CCG	CGG	TTG	TTT	AAT	ACC	AGA	TCA	GAA	ACC	CCG	GTA	TGG	GCG	GCA	CGG	3408
	Ala	Arg	Leu	Phe	Asn	Thr	Arg	Ser	Glu	Ser	Pro	Val	Trp	Ala	Ala	Arg	
				1125					1130					1135			
	CAA	GGT	TAT	ACC	GAT	TAC	GGT	GAC	GCC	GCA	CAG	TTC	TGG	CGG	CCT	CAG	3456
	Gln	Gly	Tyr	Thr	Asp	Tyr	Gly	Asp	Ala	Ala	Gln	Phe	Trp	Arg	Pro	Gln	
				1140				1145					1150				
45	GCT	CAG	CGT	AAC	TCG	TTG	CTG	ACA	GGG	AAA	ACC	ACA	CTG	ACC	TGG	GAT	3504
	Ala	Gln	Arg	Asn	Ser	Leu	Leu	Thr	Gly	Lys	Thr	Thr	Leu	Thr	Trp	Asp	
			1155					1160					1165				
50	ACC	CAT	CAT	TGT	GTA	ATA	ATA	CAG	ACT	CAA	GAT	GCC	GCT	GGA	TTA	ACG	3552
	Thr	His	His	Cys	Val	Ile	Ile	Gln	Thr	Gln	Asp	Ala	Ala	Gly	Leu	Thr	
		1170					1175					1180					
55	ACG	CAA	GCC	CAT	TAC	GAT	TAT	CGT	TTC	CTT	ACA	CCG	GTA	CAA	CTG	ACA	3600
	Thr	Gln	Ala	His	Tyr	Asp	Tyr	Arg	Phe	Leu	Thr	Pro	Val	Gln	Leu	Thr	
	1185					1190					1195				1200		
60	GAT	ATT	AAT	GAT	AAT	CAA	CAT	ATT	GTG	ACT	CTG	GAC	GCG	CTA	GGT	CGC	3648
	Asp	Ile	Asn	Asp	Asn	Gln	His	Ile	Val	Thr	Leu	Asp	Ala	Leu	Gly	Arg	
				1205					1210					1215			
	GTA	ACC	ACC	AGC	CGG	TTC	TGG	GCC	ACA	GAG	GCA	GGA	CAA	GCC	GCA	GGC	3696
	Val	Thr	Thr	Ser	Arg	Phe	Trp	Gly	Thr	Glu	Ala	Gly	Gln	Ala	Ala	Gly	
				1220				1225					1230				
65	TAT	TCC	AAC	CAG	CCC	TTC	ACA	CCA	CCG	GAC	TCC	GTA	GAT	AAA	GCG	CTG	3744
	Tyr	Ser	Asn	Gln	Pro	Phe	Thr	Pro	Pro	Asp	Ser	Val	Asp	Lys	Ala	Leu	

	1235	1240	1245	
5	GCA TTA ACC GGC GCA CTC CCT GTT GCC CAA TGT TTA GTC TAT GCG GTT 3790 Ala Leu Thr Gly Ala Leu Pro Val Ala Gln Cys Leu Val Tyr Ala Val 1250 1255 1260			
10	GAT AGC TGG ATG CCG TCG TTA TCT TTG TCT CAG CTT TCT CAG TCA CAA 3840 Asp Ser Trp Met Pro Ser Leu Ser Leu Ser Gln Leu Ser Gln Ser Gln 1265 1270 1275 1280			
	GAA GAG GCA GAA GCG CTA TGG JCG CAA CTG CGT GCC GCT CAT ATG ATT 3888 Glu Glu Ala Glu Ala Leu Trp Ala Gln Leu Arg Ala Ala His Met Ile 1285 1290 1295			
15	ACC GAA GAT GGG AAA GTG TGT GCG TTA AGC GGG AAA CGA GGA ACA AGC 3936 Thr Glu Asp Gly Lys Val Cys Ala Leu Ser Gly Lys Arg Gly Thr Ser 1300 1305 1310			
20	CAT CAG AAC CTG ACG ATT CAA CTT ATT TCG CTA TTG GCA AGT ATT CCC 3984 His Gln Asn Leu Thr Ile Gln Leu Ile Ser Leu Leu Ala Ser Ile Pro 1315 1320 1325			
25	CGT TTA CCG CCA CAT GTA CTG GGG ATC ACC ACT GAT CGC TAT GAT AGC 4032 Arg Leu Pro Pro His Val Leu Gly Ile Thr Thr Asp Arg Tyr Asp Ser 1330 1335 1340			
30	GAT CCG CAA CAG CAG CAC CAA CAG ACG GTG AGC TTT AGT GAC GGT TTT 4080 Asp Pro Gln Gln Gln His Gln Gln Thr Val Ser Phe Ser Asp Gly Phe 1345 1350 1355 1360			
	GGC CGG TTA CTC CAG AGT TCA GCT CGT CAT GAG TCA GGT GAT GCC TGG 4128 Gly Arg Leu Leu Gln Ser Ser Ala Arg His Glu Ser Gly Asp Ala Trp 1365 1370 1375			
35	CAA CGT AAA GAG GAT GCC GGG CTG GTC GTG GAT GCA AAT GGC GTT CTG 4176 Gln Arg Lys Glu Asp Gly Gly Leu Val Val Asp Ala Asn Gly Val Leu 1380 1385 1390			
40	GTC AGT GCC CCT ACA GAC ACC CGA TGG GCC GTT TCC GGT CGC ACA GAA 4224 Val Ser Ala Pro Thr Asp Thr Arg Trp Ala Val Ser Gly Arg Thr Glu 1395 1400 1405			
45	TAT GAC GAC AAA GGC CAA CCT GTG CGT ACT TAT CAA CCC TAT TTT CTA 4272 Tyr Asp Asp Lys Gly Gln Pro Val Arg Thr Tyr Gln Pro Tyr Phe Leu 1410 1415 1420			
50	AAT GAC TGG CGT TAC GTT AGT GAT GAC AGC GCA CGA GAT GAC CTG TTT 4320 Asn Asp Trp Arg Tyr Val Ser Asp Asp Ser Ala Arg Asp Asp Leu Phe 1425 1430 1435 1440			
	GCC GAT ACC CAC CTT TAT GAT CCA TTG GGA CGG GAA TAC AAA GTC ATC 4368 Ala Asp Thr His Leu Tyr Asp Pro Leu Gly Arg Glu Tyr Lys Val Ile 1445 1450 1455			
55	ACT GCT AAG AAA TAT TTG CGA GAA AAG CTG TAC ACC CCG TGG TTT ATT 4416 Thr Ala Lys Lys Tyr Leu Arg Glu Lys Leu Tyr Thr Pro Trp Phe Ile 1460 1465 1470			
60	GTC AGT GAG GAT GAA AAC GAT ACA CCA TCA AGA ACC CCA TAG 4458 Val Ser Glu Asp Glu Asn Asp Thr Ala Ser Arg Thr Pro 1475 1480 1485			

65 (2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1486 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

10

Met Gln Asp Ser Pro Glu Val Ser Ile Thr Thr Leu Ser Leu Pro Lys
 1 5 10 15

15

Gly Gly Gly Ala Ile Asn Gly Met Gly Glu Ala Leu Asn Ala Ala Gly
 20 25 30

Pro Asp Gly Met Ala Ser Leu Ser Leu Pro Leu Pro Leu Ser Thr Gly
 35 40 45

20

Arg Gly Thr Ala Pro Gly Leu Ser Leu Ile Tyr Ser Asn Ser Ala Gly
 50 55 60

25

Asn Gly Pro Phe Gly Ile Gly Trp Gln Cys Gly Val Met Ser Ile Ser
 65 70 75 80

Arg Arg Thr Gln His Gly Ile Pro Gln Tyr Gly Asn Asp Asp Thr Phe
 85 90 95

30

Leu Ser Pro Gln Gly Glu Val Met Asn Ile Ala Leu Asn Asp Gln Gly
 100 105 110

Gln Pro Asp Ile Arg Gln Asp Val Lys Thr Leu Gln Gly Val Thr Leu
 115 120 125

35

Pro Ile Ser Tyr Thr Val Thr Arg Tyr Gln Ala Arg Gln Ile Leu Asp
 130 135 140

40

Phe Ser Lys Ile Glu Tyr Trp Gln Pro Ala Ser Gly Gln Glu Gly Arg
 145 150 155 160

Ala Phe Trp Leu Ile Ser Thr Pro Asp Gly His Leu His Ile Leu Gly
 165 170 175

45

Lys Thr Ala Gln Ala Cys Leu Ala Asn Pro Gln Asn Asp Gln Gln Ile
 180 185 190

Ala Gln Trp Leu Leu Glu Glu Thr Val Thr Pro Ala Gly Glu His Val
 195 200 205

50

Ser Tyr Gln Tyr Arg Ala Glu Asp Glu Ala His Cys Asp Asp Asn Glu
 210 215 220

55

Lys Thr Ala His Pro Asn Val Thr Ala Gln Arg Tyr Leu Val Gln Val
 225 230 235 240

Asn Tyr Gly Asn Ile Lys Pro Gln Ala Ser Leu Phe Val Leu Asp Asn
 245 250 255

60

Ala Pro Pro Ala Pro Glu Glu Trp Leu Phe His Leu Val Phe Asp His
 260 265 270

Gly Glu Arg Asp Thr Ser Leu His Thr Val Pro Thr Trp Asp Ala Gly
 275 280 285

65

Thr Ala Gln Trp Ser Val Arg Pro Asp Ile Phe Ser Arg Tyr Glu Tyr

	290	295	300
5	Gly Phe Glu Val Arg Thr Arg Arg Leu Cys Gln Gln Val Leu Met Phe 305 310 315 320		
	His Arg Thr Ala Leu Met Ala Gly Glu Ala Ser Thr Asn Asp Ala Pro 325 330 335		
10	Glu Leu Val Gly Arg Leu Ile Leu Glu Tyr Asp Lys Asn Ala Ser Val 340 345 350		
	Thr Thr Leu Ile Thr Ile Arg Gln Leu Ser His Glu Ser Asp Gly Arg 355 360 365		
15	Pro Val Thr Gln Pro Pro Leu Glu Leu Ala Trp Gln Arg Phe Asp Leu 370 375 380		
	Glu Lys Ile Pro Thr Trp Gln Arg Phe Asp Ala Leu Asp Asn Phe Asn 385 390 395 400		
20	Ser Gln Gln Arg Tyr Gln Leu Val Asp Leu Arg Gly Glu Gly Leu Pro 405 410 415		
	Gly Met Leu Tyr Gln Asp Arg Gly Ala Trp Trp Tyr Lys Ala Pro Gln 420 425 430		
25	Arg Gln Glu Asp Gly Asp Ser Asn Ala Val Thr Tyr Asp Lys Ile Ala 435 440 445		
30	Pro Leu Pro Thr Leu Pro Asn Leu Gln Asp Asn Ala Ser Leu Met Asp 450 455 460		
	Ile Asn Gly Asp Gly Gln Leu Asp Trp Val Val Thr Ala Ser Gly Ile 465 470 475 480		
35	Arg Gly Tyr His Ser Gln Gln Pro Asp Gly Lys Trp Thr His Phe Thr 485 490 495		
40	Pro Ile Asn Ala Leu Pro Val Glu Tyr Phe His Pro Ser Ile Gln Phe 500 505 510		
	Ala Asp Leu Thr Gly Ala Gly Leu Ser Asp Leu Val Leu Ile Gly Pro 515 520 525		
45	Lys Ser Val Arg Leu Tyr Ala Asn Gln Arg Asn Gly Trp Arg Lys Gly 530 535 540		
	Glu Asp Val Pro Gln Ser Thr Gly Ile Thr Leu Pro Val Thr Gly Thr 545 550 555 560		
50	Asp Ala Arg Lys Leu Val Ala Phe Ser Asp Met Leu Gly Ser Gly Gln 565 570 575		
	Gln His Leu Val Glu Ile Lys Gly Asn Arg Val Thr Cys Trp Pro Asn 580 585 590		
55	Leu Gly His Gly Arg Phe Gly Gln Pro Leu Thr Leu Ser Gly Phe Ser 595 600 605		
60	Gln Pro Glu Asn Ser Phe Asn Pro Glu Arg Leu Phe Leu Ala Asp Ile 610 615 620		
	Asp Gly Ser Gly Thr Thr Asp Leu Ile Tyr Ala Gln Ser Gly Ser Leu 625 630 635 640		
65	Leu Ile Tyr Leu Asn Gln Ser Gly Asn Gln Phe Asp Ala Pro Leu Thr		

545 650 655
 Leu Ala Leu Pro Glu Gly Val Gln Phe Asp Asn Thr Cys Gln Leu Gln
 550 665 670
 5 Val Ala Asp Ile Gln Gly Leu Gly Ile Ala Ser Leu Ile Leu Thr Val
 675 680 685
 10 Pro His Ile Ala Pro His His Trp Arg Cys Asp Leu Ser Leu Thr Lys
 690 695 700
 Pro Trp Leu Leu Asn Val Met Asn Asn Asn Arg Gly Ala His His Thr
 705 710 715 720
 15 Leu His Tyr Arg Ser Ser Ala Gln Phe Trp Leu Asp Glu Lys Leu Gln
 725 730 735
 Leu Thr Lys Ala Gly Lys Ser Pro Ala Cys Tyr Leu Pro Phe Pro Met
 740 745 750
 20 His Leu Leu Trp Tyr Thr Glu Ile Gln Asp Glu Ile Ser Gly Asn Arg
 755 760 765
 25 Leu Thr Ser Glu Val Asn Tyr Ser His Gly Val Trp Asp Gly Lys Glu
 770 775 780
 Arg Glu Phe Arg Gly Phe Gly Cys Ile Lys Gln Thr Asp Thr Thr Thr
 785 790 795 800
 30 Phe Ser His Gly Thr Ala Pro Glu Gln Ala Ala Pro Ser Leu Ser Ile
 805 810 815
 Ser Trp Phe Ala Thr Gly Met Asp Glu Val Asp Ser Gln Leu Ala Thr
 820 825 830
 35 Glu Tyr Trp Gln Ala Asp Thr Gln Ala Tyr Ser Gly Phe Glu Thr Arg
 835 840 845
 Tyr Thr Val Trp Asp His Thr Asn Gln Thr Asp Gln Ala Phe Thr Pro
 850 855 860
 Asn Glu Thr Gln Arg Asn Trp Leu Thr Arg Ala Leu Lys Gly Gln Leu
 865 870 875 880
 45 Leu Arg Thr Glu Leu Tyr Gly Leu Asp Gly Thr Asp Lys Gln Thr Val
 885 890 895
 Pro Tyr Thr Val Ser Glu Ser Arg Tyr Gln Val Arg Ser Ile Pro Val
 900 905 910
 50 Asn Lys Glu Thr Glu Leu Ser Ala Trp Val Thr Ala Ile Glu Asn Arg
 915 920 925
 Ser Tyr His Tyr Glu Arg Ile Ile Thr Asp Pro Gln Phe Ser Gln Ser
 930 935 940
 55 Ile Lys Leu Gln His Asp Ile Phe Gly Gln Ser Leu Gln Ser Val Asp
 945 950 955 960
 60 Ile Ala Trp Pro Arg Arg Glu Lys Pro Ala Val Asn Pro Tyr Pro Pro
 965 970 975
 Thr Leu Pro Glu Thr Leu Phe Asp Ser Ser Tyr Asp Asp Gln Gln Gln
 980 985 990
 65 Leu Leu Arg Leu Val Arg Gln Lys Asn Ser Trp His His Leu Thr Asp

395 1000 1005
 Gly Glu Asn Trp Arg Leu Gly Leu Pro Asn Ala Gln Arg Arg Asp Val
 1010 1015 1020
 5 Tyr Thr Tyr Asp Arg Ser Lys Ile Pro Thr Glu Gly Ile Ser Leu Glu
 1025 1030 1035 1040
 10 Ile Leu Leu Lys Asp Asp Gly Leu Leu Ala Asp Glu Lys Ala Ala Val
 1045 1050 1055
 Tyr Leu Gly Gln Gln Gln Thr Phe Tyr Thr Ala Gly Gln Ala Glu Val
 1060 1065 1070
 15 Thr Leu Glu Lys Pro Thr Leu Gln Ala Leu Val Ala Phe Gln Glu Thr
 1075 1080 1085
 Ala Met Met Asp Asp Thr Ser Leu Gln Ala Tyr Glu Gly Val Ile Glu
 1090 1095 1100
 20 Glu Gln Glu Leu Asn Thr Ala Leu Thr Gln Ala Gly Tyr Gln Gln Val
 1105 1110 1115 1120
 25 Ala Arg Leu Phe Asn Thr Arg Ser Glu Ser Pro Val Trp Ala Ala Arg
 1125 1130 1135
 Gln Gly Tyr Thr Asp Tyr Gly Asp Ala Ala Gln Phe Trp Arg Pro Gln
 1140 1145 1150
 30 Ala Gln Arg Asn Ser Leu Leu Thr Gly Lys Thr Thr Leu Thr Trp Asp
 1155 1160 1165
 Thr His His Cys Val Ile Ile Gln Thr Gln Asp Ala Ala Gly Leu Thr
 1170 1175 1180
 35 Thr Gln Ala His Tyr Asp Tyr Arg Phe Leu Thr Pro Val Gln Leu Thr
 1185 1190 1195 1200
 40 Asp Ile Asn Asp Asn Gln His Ile Val Thr Leu Asp Ala Leu Gly Arg
 1205 1210 1215
 Val Thr Thr Ser Arg Phe Trp Gly Thr Glu Ala Gly Gln Ala Ala Gly
 1220 1225 1230
 45 Tyr Ser Asn Gln Pro Phe Thr Pro Pro Asp Ser Val Asp Lys Ala Leu
 1235 1240 1245
 Ala Leu Thr Gly Ala Leu Pro Val Ala Gln Cys Leu Val Tyr Ala Val
 1250 1255 1260
 50 Asp Ser Trp Met Pro Ser Leu Ser Leu Ser Gln Leu Ser Gln Ser Gln
 1265 1270 1275 1280
 55 Glu Glu Ala Glu Ala Leu Trp Ala Gln Leu Arg Ala Ala His Met Ile
 1285 1290 1295
 Thr Glu Asp Gly Lys Val Cys Ala Leu Ser Gly Lys Arg Gly Thr Ser
 1300 1305 1310
 60 His Gln Asn Leu Thr Ile Gln Leu Ile Ser Leu Leu Ala Ser Ile Pro
 1315 1320 1325
 Arg Leu Pro Pro His Val Leu Gly Ile Thr Thr Asp Arg Tyr Asp Ser
 1330 1335 1340
 65 Asp Pro Gln Gln Gln His Gln Gln Thr Val Ser Phe Ser Asp Gly Phe

1345 1350 1355 1360
 Gly Arg Leu Leu Gln Ser Ser Ala Arg His Glu Ser Gly Asp Ala Trp
 1365 1370 1375
 5 Gln Arg Lys Glu Asp Gly Gly Leu Val Val Asp Ala Asn Gly Val Leu
 1380 1385 1390
 10 Val Ser Ala Pro Thr Asp Thr Arg Trp Ala Val Ser Gly Arg Thr Glu
 1395 1400 1405
 Tyr Asp Asp Lys Gly Gln Pro Val Arg Thr Tyr Gln Pro Tyr Phe Leu
 1410 1415 1420
 15 Asn Asp Trp Arg Tyr Val Ser Asp Asp Ser Ala Arg Asp Asp Leu Phe
 1425 1430 1435 1440
 Ala Asp Thr His Leu Tyr Asp Pro Leu Gly Arg Glu Tyr Lys Val Ile
 1445 1450 1455
 20 Thr Ala Lys Lys Tyr Leu Arg Glu Lys Leu Tyr Thr Pro Trp Phe Ile
 1460 1465 1470
 25 Val Ser Glu Asp Glu Asn Asp Thr Ala Ser Arg Thr Pro
 1475 1480 1485

(2) INFORMATION FOR SEQ ID NO:33:
 (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 3288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
 40 ATG GTG ACT GTT ATG CAA AAT AAA ATA TCA TTT TTA TCA GGT ACA TCC 48
 Met Val Thr Val Met Gln Asn Lys Ile Ser Phe Leu Ser Gly Thr Ser
 1 5 10 15
 45 GAA CAG CCC CTG CTT GAC GCC GGT TAT CAA AAC GTA TTT GAT ATC GCA 96
 Glu Gln Pro Leu Leu Asp Ala Gly Tyr Gln Asn Val Phe Asp Ile Ala
 20 25 30
 50 TCA ATC AGC CCG GCT ACT TTC GTT CAA TCC GTT CCC ACC CTG CCC GTT 144
 Ser Ile Ser Arg Ala Thr Phe Val Gln Ser Val Pro Thr Leu Pro Val
 35 40 45
 55 AAA GAG GCT CAT ACC GTC TAT CGT CAG GCG CCG CAA CGT GCG GAA AAT 192
 Lys Glu Ala His Thr Val Tyr Arg Gln Ala Arg Gln Arg Ala Glu Asn
 50 55 60
 60 CTG AAA TCC CTC TAC CGA GCC TGG CAA TTG CGT CAG GAG CCG GTT ATT 240
 Leu Lys Ser Leu Tyr Arg Ala Trp Gln Leu Arg Gln Glu Pro Val Ile
 65 70 75 80
 65 AAA GGG CTG GCT AAA CTT AAC CTA CAA TCC AAC GTT TCT GTG CTT CAA 288
 Lys Gly Leu Ala Lys Leu Asn Leu Gln Ser Asn Val Ser Val Leu Gln
 85 90 95
 GAT GCT TTG GTA GAG AAT ATT GGC GGT GAT GGG GAT TTC AGC GAT TTA 336
 65 Asp Ala Leu Val Glu Asn Ile Gly Gly Asp Gly Asp Phe Ser Asp Leu

	100	105	110	
5	ATG AAC CGT GCC AGT CAA TAT GCT GAC GCT GCC TCT ATT CAA TCC CTA Met Asn Arg Ala Ser Gln Tyr Ala Asp Ala Ala Ser Ile Gln Ser Leu 115 120 125			334
10	TTT TCA CCG GGC CGT TAT GCT TCC GCA CTC TAC AGA GTT GCT AAA GAT Phe Ser Pro Gly Arg Tyr Ala Ser Ala Leu Tyr Arg Val Ala Lys Asp 130 135 140			432
15	CTG CAT AAA TCA GAT TCC AGT TTG CAT ATT GAT AAT CGC CGC GCT GAT Leu His Lys Ser Asp Ser Ser Leu His Ile Asp Asn Arg Arg Ala Asp 145 150 155 160			480
20	CTG AAG GAT CTG ATA TTA AGC GAA ACG ACG ATG AAT AAA GAG GTC ACT Leu Lys Asp Leu Ile Leu Ser Glu Thr Thr Met Asn Lys Glu Val Thr 165 170 175			528
25	TCC CTT GAT ATC TTG TTG GAT GTG CTA CAA AAA GGC GGT AAA GAT ATT Ser Leu Asp Ile Leu Leu Asp Val Leu Gln Lys Gly Gly Lys Asp Ile 180 185 190			576
30	ACT GAG CTG TCC GGC GCA TTC TTC CCA ATG ACG TTA CCT TAT GAC GAT Thr Glu Leu Ser Gly Ala Phe Phe Pro Met Thr Leu Pro Tyr Asp Asp 195 200 205			624
35	CAT CTG TCG CAA ATC GAT TCC GCT TTA TCG GCA CAA GCC AGA ACG CTG His Leu Ser Gln Ile Asp Ser Ala Leu Ser Ala Gln Ala Arg Thr Leu 210 215 220			672
40	AAC GGT GTG TGG AAT ACT TTG ACA GAT ACC ACG GCA CAA GCG GTT TCA Asn Gly Val Trp Asn Thr Leu Thr Asp Thr Thr Ala Gln Ala Val Ser 225 230 235 240			720
45	GAA CAA ACC AGT AAT ACG AAT ACA CGC AAA CTG TTC GCT GCC CAA GAT Glu Gln Thr Ser Asn Thr Asn Thr Arg Lys Leu Phe Ala Ala Gln Asp 245 250 255			768
50	GGT AAT CAA GAT ACA TTT TTT TCC GGA AAC ACT TTT TAT TTC AAA GCG Gly Asn Gln Asp Thr Phe Phe Ser Gly Asn Thr Phe Tyr Phe Lys Ala 260 265 270			816
55	GTG GGA TTC AGC GGG CAA CCT ATG GTT TAC CTG TCA CAG TAC ACC AGC Val Gly Phe Ser Gly Gln Pro Met Val Tyr Leu Ser Gln Tyr Thr Ser 275 280 285			864
60	GGG AAC GGC ATT GTC GGC GCA CAA TTG ATT GCA GGT AAT CCA GAC CAA Gly Asn Gly Ile Val Gly Ala Gln Leu Ile Ala Gly Asn Pro Asp Gln 290 295 300			912
65	GCC GCC GCC GCA ATA GTC GCA CCG TTG AAA CTC ACT TGG TCA ATG GCA Ala Ala Ala Ala Ile Val Ala Pro Leu Lys Leu Thr Trp Ser Met Ala 305 310 315 320			960
70	AAA CAG TGT TAC TAC CTC GTC GCT CCC GAT GGT ACA ACG ATG GGA GAC Lys Gln Cys Tyr Tyr Leu Val Ala Pro Asp Gly Thr Thr Met Gly Asp 325 330 335			1008
75	GGT AAT GTT CTG ACC GGC TGT TTC TTA AGA GGC AAC AGC CCA ACT AAC Gly Asn Val Leu Thr Gly Cys Phe Leu Arg Gly Asn Ser Pro Thr Asn 340 345 350			1056
80	CCG GAT AAA GAC GGT ATT TTT GCT CAG GTA GCC AAC AAA TCA GGC ACT Pro Asp Lys Asp Gly Ile Phe Ala Gln Val Ala Asn Lys Ser Gly Ser 355 360 365			1104

	ACT CAG CCT TTG CCA AGC TTC CAT CTG CCG GTC ACA CTG GAA CAC AGC	1152
	Thr Gln Pro Leu Pro Ser Phe His Leu Pro Val Thr Leu Glu His Ser	
	370 375 380	
5	GAG AAT AAA GAT CAG TAC TAT CTG AAA ACA GAG CAG GGT TAT ATC ACG	1200
	Glu Asn Lys Asp Gln Tyr Tyr Leu Lys Thr Glu Gln Gly Tyr Ile Thr	
	385 390 395 400	
10	GTA GAT AGT TCC GGA CAG TCA AAT TGG AAA AAC GCG CTG GTT ATC AAT	1248
	Val Asp Ser Ser Gly Gln Ser Asn Trp Lys Asn Ala Leu Val Ile Asn	
	405 410 415	
15	GGG ACA AAA GAC AAG GGG CTG TTA TTA ACC TTT TGC AGC GAT AGC TCA	1296
	Gly Thr Lys Asp Lys Gly Leu Leu Leu Thr Phe Cys Ser Asp Ser Ser	
	420 425 430	
20	GGC ACT CCG ACA AAC CCT GAT GAT GTG ATT CCT CCC GCT ATC AAT GAT	1344
	Gly Thr Pro Thr Asn Pro Asp Asp Val Ile Pro Pro Ala Ile Asn Asp	
	435 440 445	
25	ATT CCA TCG CCG CCA GCC CGC GAA ACA CTG TCA CTG ACG CCG GTC AGT	1392
	Ile Pro Ser Pro Pro Ala Arg Glu Thr Leu Ser Leu Thr Pro Val Ser	
	450 455 460	
30	TAT CAA TTG ATG ACC AAT CCG GCA CCG ACA GAA GAT GAT ATT ACC AAC	1440
	Tyr Gln Leu Met Thr Asn Pro Ala Pro Thr Glu Asp Asp Ile Thr Asn	
	465 470 475 480	
35	CAT TAT GGT TTT AAC GGC GCT AGC TTA CGG GCT TCT CCA TTG TCA ACC	1488
	His Tyr Gly Phe Asn Gly Ala Ser Leu Arg Ala Ser Pro Leu Ser Thr	
	485 490 495	
40	AGC GAG TTG ACC AGC AAA CTG AAT TCT ATC GAT ACT TTC TGT GAG AAG	1536
	Ser Glu Leu Thr Ser Lys Leu Asn Ser Ile Asp Thr Phe Cys Glu Lys	
	500 505 510	
45	ACC CGG TTA AGC TTC AAT CAG TTA ATG GAT TTG ACC GCT CAG CAA TCT	1584
	Thr Arg Leu Ser Phe Asn Gln Leu Met Asp Leu Thr Ala Gln Gln Ser	
	515 520 525	
50	TAC AGT CAA AGC AGC ATT GAT GCG AAA GCA GCC AGC CGC TAT GTT CGT	1632
	Tyr Ser Gln Ser Ser Ile Asp Ala Lys Ala Ala Ser Arg Tyr Val Arg	
	530 535 540	
55	TTT GGG GAA ACC ACC CCA ACC CGC GTC AAT GTC TAC GGT GCC GCT TAT	1680
	Phe Gly Glu Thr Thr Pro Thr Arg Val Asn Val Tyr Gly Ala Ala Tyr	
	545 550 555 560	
60	CTG AAC AGC ACA CTG GCA GAC GCG GCT GAT GGT CAA TAT CTG TGG ATT	1728
	Leu Asn Ser Thr Leu Ala Asp Ala Ala Asp Gly Gln Tyr Leu Trp Ile	
	565 570 575	
65	CAG ACT GAT GGC AAG AGC CTA AAT TTC ACT GAC GAT ACG GTA GTC GCC	1776
	Gln Thr Asp Gly Lys Ser Leu Asn Phe Thr Asp Asp Thr Val Val Ala	
	580 585 590	
70	TTA GCC GGT CGC GCT GAA AAG CTG GTA CGT TTA TCA TCC CAG ACC GGG	1824
	Leu Ala Gly Arg Ala Glu Lys Leu Val Arg Leu Ser Ser Gln Thr Gly	
	595 600 605	
75	CTA TCA TTT GAA GAA TTG GAC TGG CTG ATT GCC AAT GCC AGT CGT AGT	1872
	Leu Ser Phe Glu Glu Leu Asp Trp Leu Ile Ala Asn Ala Ser Arg Ser	
	610 615 620	
80	GTG CCG GAC CAC CAC GAC AAA ATT GTG CTG GAT AAG CCG GTC CTT GAA	1920
	Val Pro Asp His His Asp Lys Ile Val Leu Asp Lys Pro Val Leu Glu	

	625	630	635	640	
5	GCA CTG GCA GAG TAT GTC AGC CTA AAA CAG CCC TAT GGG CTT GAT GCC Ala Leu Ala Glu Tyr Val Ser Leu Lys Gln Arg Tyr Gly Leu Asp Ala 645 650 655	1963			
10	AAT ACC TTT GCG ACC TTC ATT AGT CCA GTA AAT CCT TAT ACG CCA GAT Asn Thr Phe Ala Thr Phe Ile Ser Ala Val Asn Pro Tyr Thr Pro Asp 660 665 670	2015			
15	CAG ACA CCC AGT TTC TAT GAA ACC GCT TTC CGC TCT GCC GAC GGT AAT Gln Thr Pro Ser Phe Tyr Glu Thr Ala Phe Arg Ser Ala Asp Gly Asn 675 680 685	2064			
20	CAT GTC ATT GCG CTA GGT ACA GAG GTG AAA TAT GCA GAA AAT GAG CAG His Val Ile Ala Leu Gly Thr Glu Val Lys Tyr Ala Glu Asn Glu Gln 690 695 700	2112			
25	GAT GAG TTA GCC GCC ATA TGC TGC AAA GCA TTG GGT GTC ACC AGT GAT Asp Glu Leu Ala Ala Ile Cys Cys Lys Ala Leu Gly Val Thr Ser Asp 705 710 715 720	2160			
30	GAA CTG CTC CGT ATT GGT CGC TAT TGC TTC GGT AAT GCA GGC AGT TTT Glu Leu Leu Arg Ile Gly Arg Tyr Cys Phe Gly Asn Ala Gly Ser Phe 725 730 735	2208			
35	ACC TTG GAT GAA TAT ACC GCC AGT CAG TTG TAT CGC TTC GGC GCC ATT Thr Leu Asp Glu Tyr Thr Ala Ser Gln Leu Tyr Arg Phe Gly Ala Ile 740 745 750	2256			
40	CCC CGT TTG TTT GGG CTG ACA TTT GCC CAA GCC GAA ATT TTA TCG CGT Pro Arg Leu Phe Gly Leu Thr Phe Ala Gln Ala Glu Ile Leu Trp Arg 755 760 765	2304			
45	CTG ATG GAA GGC GGA AAA GAT ATC TTA TTG CAA CAG TTA GGT CAG GCA Leu Met Glu Gly Gly Lys Asp Ile Leu Leu Gln Gln Leu Gly Gln Ala 770 775 780	2352			
50	AAA TCC CTG CAA CCA CTG GCT ATT TTA CGC CGT ACC GAG CAG GTG CTG Lys Ser Leu Gln Pro Leu Ala Ile Leu Arg Arg Thr Glu Gln Val Leu 785 790 795 800	2400			
55	GAT TGG ATG TCG TCC GTA AAT CTA AGT CTG ACT TAT CTG CAA GGG ATG Asp Trp Met Ser Ser Val Asn Leu Ser Leu Thr Tyr Leu Gln Gly Met 805 810 815	2448			
60	GTA AGT ACG CAA TGG AGC GGT ACC GCC ACC GCT GAG ATG TTC AAT TTC Val Ser Thr Gln Trp Ser Gly Thr Ala Thr Ala Glu Met Phe Asn Phe 820 825 830	2496			
65	TTG GAA AAC GTT TGT GAC AGC GTG AAT AGT CAA GCT GCC ACT AAA GAA Leu Glu Asn Val Cys Asp Ser Val Asn Ser Gln Ala Ala Thr Lys Glu 835 840 845	2544			
70	ACA ATG GAT TCG GCG TTA CAG CAG AAA GTG CTG CGG GCG CTA AGC GCC Thr Met Asp Ser Ala Leu Gln Gln Lys Val Leu Arg Ala Leu Ser Ala 850 855 860	2592			
75	GGT TTC GGC ATT AAG AGC AAT GTG ATG GGT ATC GTC ACC TTC TGG CTG Gly Phe Gly Ile Lys Ser Asn Val Met Gly Ile Val Thr Phe Trp Leu 865 870 875 880	2640			
80	GAG AAA ATC ACA ATC GGT AGT GAT AAT CCT TTT ACA TTG GCA AAC TAC Glu Lys Ile Thr Ile Gly Ser Asp Asn Pro Phe Thr Leu Ala Asn Tyr 885 890 895	2688			

TGG CAT GAT ATT CAA ACC CTG TTT AGC CAT GAC AAT GCC ACG TTA GAG 2734
 Trp His Asp Ile Gln Thr Leu Phe Ser His Asp Asn Ala Thr Leu Glu
 900 905 910

5 TCC TTA CAA ACC GAC ACT TCT CTG GTA ATT GCT ACT CAG CAA CTT AGC 2784
 Ser Leu Gln Thr Asp Thr Ser Leu Val Ile Ala Thr Gln Gln Leu Ser
 915 920 925

10 CAG CTA GTG TTA ATT GTG AAA TGG CTG AGC CTG ACC GAG CAG GAT CTG 2832
 Gln Leu Val Leu Ile Val Lys Trp Leu Ser Leu Thr Glu Gln Asp Leu
 930 935 940

15 CAA TTA CTG ACA ACC TAT CCC GAA CGT TTA ATC AAC GGC ATC ACG AAT 2880
 Gln Leu Leu Thr Thr Tyr Pro Glu Arg Leu Ile Asn Gly Ile Thr Asn
 945 950 955 960

20 GTT CCT GTA CCC AAT CCG GAG CTA TTA CTC ACG CTA TCA CGT TTT AAG 2923
 Val Pro Val Pro Asn Pro Glu Leu Leu Leu Thr Leu Ser Arg Phe Lys
 965 970 975

CAG TGG GAA ACT CAA GTC ACC GTT TCC CGT GAT GAA GCG ATG CGC TGT 2976
 Gln Trp Glu Thr Gln Val Thr Val Ser Arg Asp Glu Ala Met Arg Cys
 980 985 990

25 TTC GAT CAA TTA AAT GCC AAT GAT ATG ACG ACT GAA AAT GCA GGT TCA 3024
 Phe Asp Gln Leu Asn Ala Asn Asp Met Thr Thr Glu Asn Ala Gly Ser
 995 1000 1005

30 CTG ATC GCC ACA TTG TAT GAG ATG GAT AAA GGT ACG GGA GCG CAA GTT 3072
 Leu Ile Ala Thr Leu Tyr Glu Met Asp Lys Gly Thr Gly Ala Gln Val
 1010 1015 1020

35 AAT ACC TTG CTA TTA GGT GAA AAT AAC TGG CCG AAA AGT TTT ACC TCT 3120
 Asn Thr Leu Leu Leu Gly Glu Asn Asn Trp Pro Lys Ser Phe Thr Ser
 1025 1030 1035 1040

40 CTC TGG CAA CTT CTG ACC TGG TTA CGC GTC GGG CAA AGA CTG AAT GTC 3168
 Leu Trp Gln Leu Leu Thr Trp Leu Arg Val Gly Gln Arg Leu Asn Val
 1045 1050 1055

GGT AGT ACC ACT CTG GGC AAT CTG TTG TCC ATG ATG CAA GCA GAC CCT 3216
 Gly Ser Thr Thr Leu Gly Asn Leu Leu Ser Met Met Gln Ala Asp Pro
 1060 1065 1070

45 GCT GCC GAG AGT AGC GCT TTA TTG GCA TCA GTA GCC CAA AAC TTA AGT 3264
 Ala Ala Glu Ser Ser Ala Leu Leu Ala Ser Val Ala Gln Asn Leu Ser
 1075 1080 1085

50 GCC GCA ATC AGC AAT CGT CAG TAA 3285
 Ala Ala Ile Ser Asn Arg Gln ...
 1090 1095

- (2) INFORMATION FOR SEQ ID NO:34:
 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1095 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
 65 Features From To Description
 254 267 SEQ ID NO:15
 254 492 Tcaa11 peptide

5 Met Val Thr Val Met Gln Asn Lys Ile Ser Phe Leu Ser Gly Thr Ser
 1 5 10 15
 Glu Gln Pro Leu Leu Asp Ala Gly Tyr Gln Asn Val Phe Asp Ile Ala
 20 25 30
 10 Ser Ile Ser Arg Ala Thr Phe Val Gln Ser Val Pro Thr Leu Pro Val
 35 40 45
 Lys Glu Ala His Thr Val Tyr Arg Gln Ala Arg Gln Arg Ala Glu Asn
 50 55 60
 15 Leu Lys Ser Leu Tyr Arg Ala Trp Gln Leu Arg Gln Glu Pro Val Ile
 65 70 75 80
 Lys Gly Leu Ala Lys Leu Asn Leu Gln Ser Asn Val Ser Val Leu Gln
 85 90 95
 20 Asp Ala Leu Val Glu Asn Ile Gly Gly Asp Gly Asp Phe Ser Asp Leu
 100 105 110
 25 Met Asn Arg Ala Ser Gln Tyr Ala Asp Ala Ala Ser Ile Gln Ser Leu
 115 120 125
 Phe Ser Pro Gly Arg Tyr Ala Ser Ala Leu Tyr Arg Val Ala Lys Asp
 130 135 140
 30 Leu His Lys Ser Asp Ser Ser Leu His Ile Asp Asn Arg Arg Ala Asp
 145 150 155 160
 Leu Lys Asp Leu Ile Leu Ser Glu Thr Thr Met Asn Lys Glu Val Thr
 165 170 175
 35 Ser Leu Asp Ile Leu Leu Asp Val Leu Gln Lys Gly Gly Lys Asp Ile
 180 185 190
 40 Thr Glu Leu Ser Gly Ala Phe Phe Pro Met Thr Leu Pro Tyr Asp Asp
 195 200 205
 His Leu Ser Gln Ile Asp Ser Ala Leu Ser Ala Gln Ala Arg Thr Leu
 210 215 220
 45 Asn Gly Val Trp Asn Thr Leu Thr Asp Thr Thr Ala Gln Ala Val Ser
 225 230 235 240
 Glu Gln Thr Ser Asn Thr Asn Thr Arg Lys Leu Phe Ala Ala Gln Asp
 245 250 255
 50 Gly Asn Gln Asp Thr Phe Phe Ser Gly Asn Thr Phe Tyr Phe Lys Ala
 260 265 270
 55 Val Gly Phe Ser Gly Gln Pro Met Val Tyr Leu Ser Gln Tyr Thr Ser
 275 280 285
 Gly Asn Gly Ile Val Gly Ala Gln Leu Ile Ala Gly Asn Pro Asp Gln
 290 295 300
 60 Ala Ala Ala Ala Ile Val Ala Pro Leu Lys Leu Thr Trp Ser Met Ala
 305 310 315 320
 Lys Gln Cys Tyr Tyr Leu Val Ala Pro Asp Gly Thr Thr Met Gly Asp
 325 330 335
 65 Gly Asn Val Leu Thr Gly Cys Phe Leu Arg Gly Asn Ser Pro Thr Asn

	340	345	350
	Pro Asp Lys Asp Gly Ile Phe Ala Gln Val Ala Asn Lys Ser Gly Ser		
	355	360	365
5	Thr Gln Pro Leu Pro Ser Phe His Leu Pro Val Thr Leu Glu His Ser		
	370	375	380
10	Glu Asn Lys Asp Gln Tyr Tyr Leu Lys Thr Glu Gln Gly Tyr Ile Thr		
	385	390	395
	Val Asp Ser Ser Gly Gln Ser Asn Trp Lys Asn Ala Leu Val Ile Asn		
	405	410	415
15	Gly Thr Lys Asp Lys Gly Leu Leu Leu Thr Phe Cys Ser Asp Ser Ser		
	420	425	430
	Gly Thr Pro Thr Asn Pro Asp Asp Val Ile Pro Pro Ala Ile Asn Asp		
	435	440	445
20	Ile Pro Ser Pro Pro Ala Arg Glu Thr Leu Ser Leu Thr Pro Val Ser		
	450	455	460
25	Tyr Gln Leu Met Thr Asn Pro Ala Pro Thr Glu Asp Asp Ile Thr Asn		
	465	470	475
	His Tyr Gly Phe Asn Gly Ala Ser Leu Arg Ala Ser Pro Leu Ser Thr		
	485	490	495
30	Ser Glu Leu Thr Ser Lys Leu Asn Ser Ile Asp Thr Phe Cys Glu Lys		
	500	505	510
	Thr Arg Leu Ser Phe Asn Gln Leu Met Asp Leu Thr Ala Gln Gln Ser		
	515	520	525
35	Tyr Ser Gln Ser Ser Ile Asp Ala Lys Ala Ala Ser Arg Tyr Val Arg		
	530	535	540
40	Phe Gly Glu Thr Thr Pro Thr Arg Val Asn Val Tyr Gly Ala Ala Tyr		
	545	550	555
	Leu Asn Ser Thr Leu Ala Asp Ala Ala Asp Gly Gln Tyr Leu Trp Ile		
	565	570	575
45	Gln Thr Asp Gly Lys Ser Leu Asn Phe Thr Asp Asp Thr Val Val Ala		
	580	585	590
	Leu Ala Gly Arg Ala Glu Lys Leu Val Arg Leu Ser Ser Gln Thr Gly		
	595	600	605
50	Leu Ser Phe Glu Glu Leu Asp Trp Leu Ile Ala Asn Ala Ser Arg Ser		
	610	615	620
55	Val Pro Asp His His Asp Lys Ile Val Leu Asp Lys Pro Val Leu Glu		
	625	630	635
	Ala Leu Ala Glu Tyr Val Ser Leu Lys Gln Arg Tyr Gly Leu Asp Ala		
	645	650	655
60	Asn Thr Phe Ala Thr Phe Ile Ser Ala Val Asn Pro Tyr Thr Pro Asp		
	660	665	670
	Gln Thr Pro Ser Phe Tyr Glu Thr Ala Phe Arg Ser Ala Asp Gly Asn		
	675	680	685
65	His Val Ile Ala Leu Gly Thr Glu Val Lys Tyr Ala Glu Asn Glu Gln		

	690	695	700
5	Asp Glu Leu Ala Ala Ile Cys Cys Lys Ala Leu Gly Val Thr Ser Asp 705 710 715 720		
	Glu Leu Leu Arg Ile Gly Arg Tyr Cys Phe Gly Asn Ala Gly Ser Phe 725 730 735		
10	Thr Leu Asp Glu Tyr Thr Ala Ser Gln Leu Tyr Arg Phe Gly Ala Ile 740 745 750		
	Pro Arg Leu Phe Gly Leu Thr Phe Ala Gln Ala Glu Ile Leu Trp Arg 755 760 765		
15	Leu Met Glu Gly Gly Lys Asp Ile Leu Leu Gln Gln Leu Gly Gln Ala 770 775 780		
	Lys Ser Leu Gln Pro Leu Ala Ile Leu Arg Arg Thr Glu Gln Val Leu 785 790 795 800		
20	Asp Trp Met Ser Ser Val Asn Leu Ser Leu Thr Tyr Leu Gln Gly Met 805 810 815		
	Val Ser Thr Gln Trp Ser Gly Thr Ala Thr Ala Glu Met Phe Asn Phe 820 825 830		
25	Leu Glu Asn Val Cys Asp Ser Val Asn Ser Gln Ala Ala Thr Lys Glu 835 840 845		
	Thr Met Asp Ser Ala Leu Gln Gln Lys Val Leu Arg Ala Leu Ser Ala 850 855 860		
30	Gly Phe Gly Ile Lys Ser Asn Val Met Gly Ile Val Thr Phe Trp Leu 865 870 875 880		
	Glu Lys Ile Thr Ile Gly Ser Asp Asn Pro Phe Thr Leu Ala Asn Tyr 885 890 895		
35	Trp His Asp Ile Gln Thr Leu Phe Ser His Asp Asn Ala Thr Leu Glu 900 905 910		
	Ser Leu Gln Thr Asp Thr Ser Leu Val Ile Ala Thr Gln Gln Leu Ser 915 920 925		
40	Gln Leu Val Leu Ile Val Lys Trp Leu Ser Leu Thr Glu Gln Asp Leu 930 935 940		
	Gln Leu Leu Thr Thr Tyr Pro Glu Arg Leu Ile Asn Gly Ile Thr Asn 945 950 955 960		
45	Val Pro Val Pro Asn Pro Glu Leu Leu Leu Thr Leu Ser Arg Phe Lys 965 970 975		
	Gln Trp Glu Thr Gln Val Thr Val Ser Arg Asp Glu Ala Met Arg Cys 980 985 990		
50	Phe Asp Gln Leu Asn Ala Asn Asp Met Thr Thr Glu Asn Ala Gly Ser 995 1000 1005		
	Leu Ile Ala Thr Leu Tyr Glu Met Asp Lys Gly Thr Gly Ala Gln Val 1010 1015 1020		
55	Asn Thr Leu Leu Leu Gly Glu Asn Asn Trp Pro Lys Ser Phe Thr Ser 1025 1030 1035 1040		
	Leu Trp Gln Leu Leu Thr Trp Leu Arg Val Gly Gln Arg Leu Asn Val		

[illegible]

(2) INFORMATION FOR SEQ ID NO:35

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 603 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

25	Pro	Leu	Ser	Thr	Ser	Glu	Leu	Thr	Ser	Lys	Leu	Asn	Ser	Ile	Asp	Thr
	1				5					10					15	
	Phe	Cys	Glu	Lys	Thr	Arg	Leu	Ser	Phe	Asn	Gln	Leu	Met	Asp	Leu	Thr
				20					25					30		
30	Ala	Gln	Gln	Ser	Tyr	Ser	Gln	Ser	Ser	Ile	Asp	Ala	Lys	Ala	Ala	Ser
			35					40					45			
	Arg	Tyr	Val	Arg	Phe	Gly	Glu	Thr	Thr	Pro	Thr	Arg	Val	Asn	Val	Tyr
35		50					55					60				
	Gly	Ala	Ala	Tyr	Leu	Asn	Ser	Thr	Leu	Ala	Asp	Ala	Ala	Asp	Gly	Gln
	65					70					75					80
	Tyr	Leu	Trp	Ile	Gln	Thr	Asp	Gly	Lys	Ser	Leu	Asn	Phe	Thr	Asp	Asp
40					85					90					95	
	Thr	Val	Val	Ala	Leu	Ala	Gly	Arg	Ala	Glu	Lys	Leu	Val	Arg	Leu	Ser
				100					105					110		
45	Ser	Gln	Thr	Gly	Leu	Ser	Phe	Glu	Glu	Leu	Asp	Trp	Leu	Ile	Ala	Asn
			115					120					125			
	Ala	Ser	Arg	Ser	Val	Pro	Asp	His	His	Asp	Lys	Ile	Val	Leu	Asp	Lys
50		130					135					140				
	Pro	Val	Leu	Glu	Ala	Leu	Ala	Glu	Tyr	Val	Ser	Leu	Lys	Gln	Arg	Tyr
	145					150					155					160
	Gly	Leu	Asp	Ala	Asn	Thr	Phe	Ala	Thr	Phe	Ile	Ser	Ala	Val	Asn	Pro
55					165					170					175	
	Tyr	Thr	Pro	Asp	Gln	Thr	Pro	Ser	Phe	Tyr	Glu	Thr	Ala	Phe	Arg	Ser
				180					185					190		
60	Ala	Asp	Gly	Asn	His	Val	Ile	Ala	Leu	Gly	Thr	Glu	Val	Lys	Tyr	Ala
		195						200					205			
	Glu	Asn	Glu	Gln	Asp	Glu	Leu	Ala	Ala	Ile	Cys	Cys	Lys	Ala	Leu	Gly
65		210					215					220				

Val Thr Ser Asp Glu Leu Leu Arg Ile Gly Arg Tyr Cys Phe Gly Asn
225 230 235 240

5 Ala Gly Arg Phe Thr Leu Asp Glu Tyr Thr Ala Ser Gln Leu Tyr Arg
245 250 255

Phe Gly Ala Ile Pro Arg Leu Phe Gly Leu Thr Phe Ala Gln Ala Glu
260 265 270

10 Ile Leu Trp Arg Leu Met Glu Gly Gly Lys Asp Ile Leu Leu Gln Gln
275 280 285

15 Xxx Gly Gln Ala Lys Ser Leu Gln Pro Leu Ala Ile Leu Arg Arg Thr
290 295 300

Glu Gln Val Leu Asp Trp Met Ser Pro Val Asn Leu Ser Leu Thr Tyr
305 310 315 320

20 Leu Gln Gly Met Val Ser Thr Gln Trp Ser Gly Thr Ala Thr Ala Glu
325 330 335

Met Phe Asn Phe Leu Glu Asn Val Cys Asp Ser Val Asn Ser Gln Ala
340 345 350

25 Xxx Thr Lys Glu Thr Met Asp Ser Ala Leu Gln Gln Lys Val Leu Arg
355 360 365

30 Ala Leu Ser Ala Gly Phe Gly Ile Lys Ser Asn Val Met Gly Ile Val
370 375 380

Thr Phe Trp Leu Glu Lys Ile Thr Ile Gly Arg Asp Asn Pro Phe Thr
385 390 395 400

35 Leu Ala Asn Tyr Trp His Asp Ile Gln Thr Leu Phe Ser His Asp Asn
405 410 415

Ala Thr Leu Glu Ser Leu Gln Thr Asp Thr Ser Leu Val Ile Ala Thr
420 425 430

40 Gln Gln Leu Ser Gln Leu Val Leu Ile Val Lys Trp Val Ser Leu Thr
435 440 445

45 Glu Gln Asp Leu Gln Leu Leu Thr Thr Tyr Pro Glu Arg Leu Ile Asn
450 455 460

Gly Ile Thr Asn Val Pro Val Pro Asn Pro Glu Leu Leu Leu Thr Leu
465 470 475 480

50 Ser Arg Phe Lys Gln Trp Glu Thr Gln Val Thr Val Ser Arg Asp Glu
485 490 495

Ala Met Arg Cys Phe Asp Gln Leu Asn Ala Asn Asp Met Thr Thr Glu
500 505 510

55 Asn Ala Gly Ser Leu Ile Ala Thr Leu Tyr Glu Met Asp Lys Gly Thr
515 520 525

60 Gly Ala Gln Val Asn Thr Leu Leu Leu Gly Glu Asn Asn Trp Pro Lys
530 535 540

Ser Phe Thr Ser Leu Trp Gln Leu Leu Thr Trp Leu Arg Val Gly Gln
545 550 555 560

65 Arg Leu Asn Val Gly Ser Thr Thr Leu Gly Asn Leu Leu Ser Met Met
565 570 575

Gln Ala Asp Pro Ala Ala Glu Ser Ser Ala Leu Leu Ala Ser Val Ala
 580 585 590

5 Gln Asn Leu Ser Ala Ala Ile Ser Asn Arg Gln
 595 600

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 2557 base pairs
 (B) TYPE: nucleic acid
 (C) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCGGCT TCGGTTTAAT ATTGATGATG TCTCGCTCTT CCGCCTGCTT AAAATTACCG 60
 20 ACCATGATAA TAAAGATGGA AAAATTAAAA ATAACCTAAA GAATCTTTCC AATTTATATA 120
 TTGGAAAATT ACTGGCAGAT ATTCATCAAT TAACCATTGA TGAAGTGGAT TTATTACTGA 180
 TTGCCGTAGG TGAAGGAAAA ACTAATTTAT CCGCTATCAG TGATAAGCAA TTGGCTACCC 240
 TGATCAGAAA ACTCAATACT ATTACCAGCT GGCTACATAC ACAGAAGTGG AGTGTATTCC 300
 AGCTATTTAT CATGACCTCC ACCAGCTATA ACAAACGCT AACGCCTGAA ATTAAGAATT 360
 25 TGCTGGATAC CGTCTACCAC GGTTTACAAG GTTTTGATAA AGACAAAGCA GATTTGCTAC 420
 ATGTCATGGC GCCCTATATT GCGGCCACCT TGCAATTATC ATCGGAAAAT GTCGCCCCACT 480
 CGGTACTCCT TTGGGCAGAT AAGTTACAGC CCGGCGACGG CGCAATGACA GCAGAGGGAN 540
 TCTGGGACTG GTTGAATACT AAGTATACGC CGGGTTTCATC GGAAGCCGTA GAAACGCAGG 600
 AACATATCGT TCAGTATTGT CAGGCTCTGG CACAATTGGA AATGGTTTAC CATTCCACCG 660
 30 GCATCAACGA AAACGCCTTC CGTCTATTTG TGACAAAACC AGAGATGTTT GGCGCTGCAA 720
 CTGGAGCAGC GCCCGCGCAT GATGCCCTTT CACTGATTAT GCTGACACGT TTTGCGGATT 780
 GGGTGAACGC ACTAGGCGAA AAAGCGTCCT CCGTGCTAGC GGCATTTGAA GCTAACTCGT 840
 TAACGGCAGA ACAACTGGCT GATGCCATGA ATCTTGATGC TAATTTGCTG TTGCAAGCCA 900
 GTATTCAAGC ACAAATCAT CAACATCTTC CCCCAGTAAC TCCAGAAAAT GCGTTCCTCT 960
 35 GTTGGACATC TATCAATACT ATCCTGCAAT GGGTTAATGT CGCACAACAA TTGAAATGTC 1020
 GCCCCACAGG GCGTTTCCGC TTTGGTCCGG CTGGATTATA TTCAATCAAT GAAAGAGACA 1080
 CCGACCTATG CCCAGTGGGA AAACGCGGCA GGCGTATTAA CCGCCGGGTT GAATTCAACA 1140
 ACAGGCTAAT ACATTACAAC GCTTTTCTGG ATGAATCTCG CAGTGCCGCA TTAAGCACCT 1200
 ACTATATCCG TCAAGTCGCC AAGGCAGCGG CCGCTATTAA AAGCCGTGAT GACTTGTATC 1260
 40 AATACTTACT GATTGATAAT CAGGTTTCTG CGGCAATAAA AACCACCCGG ATCGCCGAAG 1320
 CCATTGCCAG TATTCAACTG TACGTCAACC GGGCATTGGA AAATGTGGAA GAAAATGCCA 1380
 ATTCGGGGGT TATCAGCCGC CAATTCTTTA TCGACTGGGA CAAATACAAT AAACGCTACA 1440
 GCACTTGGGC GGGTGTCTTCT CAATTAGTTT ACTACCCGGA AAATATATT GATCCGACCA 1500
 TCGGTATCGG ACAAACCAA ATGATGGACG CATTACTGCA ATCCGTCAGC CAAAGCCAAT 1560
 45 TAAACGCCGA TACCGTCGAA GATGCCCTTA TGTCTTATCT GACATCGTTT GAACAAGTGG 1620
 CTAATCTTAA AGTTATTAGC GCATATCAGC ATAATATTAA TAACGATCAA GGGCTGACCT 1680
 ATTTTATCGG ACTCAGTGAA ACTGATGCCG GTGAATATTA TTGGCGCAGT GTCGATCACA 1740
 GTAAATTCAA CGACGGTAAA TTCGCGGCTA ATGCCTGGAG TGAATGGCAT AAAATTGATT 1800
 GTCCAATTAA CCCTTATAAA AGCACTATCC GTCCAGTGAT ATATAAATCC CGCCTGTATC 1860

TGCTCTGGTT GGAACAAAAG GAGATCACCA AACAGACAGG AAATAGTAAA GATGGCTATC 1920
 AACTGAAAC GGATTATCGT TATGAACTAA AATTGGCGCA TATCCGCTAT GATGGCACTT 1960
 GGAATACGCC AATCACCTTT GATGTCAATA AAAAAATATC CGAGCTAAAA CTGGAAAAAA 2040
 ATAGAGCGCC CGGACTCTAT TGTGCCGGTT ATCAAGGTGA AGATACGTTG CTGGTGATGT 2100
 5 TTTATAACCA ACAAGACACA CTAGATAGTT ATAAAAACGC TTCAATGCAA GGACTATATA 2160
 TCTTTGCTGA TATGGCATCC AAAGATATGA CCCCAGAACA GAGCAATGTT TATCGGGATA 2220
 ATAGCTATCA ACAATTTGAT ACCAATAATG TCAGAAGAGT GAATAACCGC TATGCAGAGG 2280
 ATTATGAGAT TCCTTCTTCG GTAAGTAGCC GTAAAGACTA TGGTTGGGGA GATTATTACC 2340
 TCAGCATGGT ATATAACGGA GATATTCCAA CTATCAATTA CAAAGCCGCA TCAAGTGATT 2400
 10 TAAAAATTTA TATTTACCA AAATTAAGAA TTATTCATAA TGGATATGAA GGACAGAAGC 2460
 GCAATCAATG CAATTTGATG AATAAATATG GCAAAC TAGG TGATAAATTT ATTGTGTATA 2520
 CCAGCCTGGG CGTTAATCCG AATAATAAGC CGAATTC 2557

- 15 (2) INFORMATION FOR SEQ ID NO:37:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 845 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
 20 (ii) MOLECULE TYPE: protein (partial)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

25 Ala Phe Asn Ile Asp Asp Val Ser Leu Phe Arg Leu Leu Lys Ile Thr
 1 5 10 15
 30 Asp His Asp Asn Lys Asp Gly Lys Ile Lys Asn Asn Leu Lys Asn Leu
 20 25 30
 Ser Asn Leu Tyr Ile Gly Lys Leu Leu Ala Asp Ile His Gln Leu Thr
 35 35 40 45
 Ile Asp Glu Leu Asp Leu Leu Leu Ile Ala Val Gly Glu Gly Lys Thr
 50 55 60
 Asn Leu Ser Ala Ile Ser Asp Lys Gln Leu Ala Thr Leu Ile Arg Lys
 40 65 70 75 80
 Leu Asn Thr Ile Thr Ser Trp Leu His Thr Gln Lys Trp Ser Val Phe
 85 90 95
 45 Gln Leu Phe Ile Met Thr Ser Thr Ser Tyr Asn Lys Thr Leu Thr Pro
 100 105 110
 Glu Ile Lys Asn Leu Leu Asp Thr Val Tyr His Gly Leu Gln Gly Phe
 115 120 125
 50 Asp Lys Asp Lys Ala Asp Leu Leu His Val Met Ala Pro Tyr Ile Ala
 130 135 140
 Ala Thr Leu Gln Leu Ser Ser Glu Asn Val Ala His Ser Val Leu Leu
 55 145 150 155 160
 Trp Ala Asp Lys Leu Gln Pro Gly Asp Gly Ala Met Thr Ala Glu Gly
 165 170 175
 Phe Trp Asp Trp Leu Asn Thr Lys Tyr Thr Pro Gly Ser Ser Glu Ala

180 185 190

5 Val Glu Thr Gln Glu His Ile Val Gln Tyr Cys Gln Ala Leu Ala Gln
195 200 205

Leu Glu Met Val Tyr His Ser Thr Gly Ile Asn Glu Asn Ala Phe Arg
210 215 220

10 Leu Phe Val Thr Lys Pro Glu Met Phe Gly Ala Ala Thr Gly Ala Ala
225 230 235 240

Pro Ala His Asp Ala Leu Ser Leu Ile Met Leu Thr Arg Phe Ala Asp
245 250 255

15 Trp Val Asn Ala Leu Gly Glu Lys Ala Ser Ser Val Leu Ala Ala Phe
260 265 270

Glu Ala Asn Ser Leu Thr Ala Glu Gln Leu Ala Asp Ala Met Asn Leu
275 280 285

20 Asp Ala Asn Leu Leu Leu Gln Ala Ser Ile Gln Ala Gln Asn His Gln
290 295 300

His Leu Pro Pro Val Thr Pro Glu Asn Ala Phe Ser Cys Trp Thr Ser
305 310 315 320

Ile Asn Thr Ile Leu Gln Trp Val Asn Val Ala Gln Gln Leu Lys Cys
325 330 335

30 Arg Pro Thr Gly Arg Phe Arg Phe Gly Arg Ala Gly Leu Tyr Ser Ile
340 345 350

Asn Glu Arg Asp Thr Asp Leu Cys Pro Val Gly Lys Arg Gly Arg Arg
355 360 365

35 Ile Asn Arg Arg Val Glu Phe Asn Asn Arg Leu Ile His Tyr Asn Ala
370 375 380

Phe Leu Asp Glu Ser Arg Ser Ala Ala Leu Ser Thr Tyr Tyr Ile Arg
385 390 395 400

Gln Val Ala Lys Ala Ala Ala Ala Ile Lys Ser Arg Asp Asp Leu Tyr
405 410 415

45 Gln Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Ala Ile Lys Thr Thr
420 425 430

Arg Ile Ala Glu Ala Ile Ala Ser Ile Gln Leu Tyr Val Asn Arg Ala
435 440 445

50 Leu Glu Asn Val Glu Glu Asn Ala Asn Ser Gly Val Ile Ser Arg Gln
450 455 460

Phe Phe Ile Asp Trp Asp Lys Tyr Asn Lys Arg Tyr Ser Thr Trp Ala
465 470 475 480

Gly Val Ser Gln Leu Val Tyr Tyr Pro Glu Asn Tyr Ile Asp Pro Thr
485 490 495

60 Met Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu Gln Ser Val
500 505 510

Ser Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala Phe Met Ser
515 520 525

65 Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val Ile Ser Ala

530 535 540

5 Tyr His Asp Asn Ile Asn Asn Asp Gln Gly Leu Thr Tyr Phe Ile Gly
545 550 555 560

Leu Ser Glu Thr Asp Ala Gly Glu Tyr Tyr Trp Arg Ser Val Asp His
565 570 575

10 Ser Lys Phe Asn Asp Gly Lys Phe Ala Ala Asn Ala Trp Ser Glu Trp
580 585 590

His Lys Ile Asp Cys Pro Ile Asn Pro Tyr Lys Ser Thr Ile Arg Pro
595 600 605

15 Val Ile Tyr Lys Ser Arg Leu Tyr Leu Leu Trp Leu Glu Gln Lys Glu
610 615 620

Ile Thr Lys Gln Thr Gly Asn Ser Lys Asp Gly Tyr Gln Thr Glu Thr
625 630 635 640

20 Asp Tyr Arg Tyr Glu Leu Lys Leu Ala His Ile Arg Tyr Asp Gly Thr
645 650 655

25 Trp Asn Thr Pro Ile Thr Phe Asp Val Asn Lys Lys Ile Ser Glu Leu
660 665 670

Lys Leu Glu Lys Asn Arg Ala Pro Gly Leu Tyr Cys Ala Gly Tyr Gln
675 680 685

30 Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Asn Gln Gln Asp Thr Leu
690 695 700

35 Asp Ser Tyr Lys Asn Ala Ser Met Gln Gly Leu Tyr Ile Phe Ala Asp
705 710 715 720

Met Ala Ser Lys Asp Met Thr Pro Glu Gln Ser Asn Val Tyr Arg Asp
725 730 735

40 Asn Ser Tyr Gln Gln Phe Asp Thr Asn Asn Val Arg Arg Val Asn Asn
740 745 750

Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Ser Ser Arg Lys
755 760 765

45 Asp Tyr Gly Trp Gly Asp Tyr Tyr Leu Ser Met Val Tyr Asn Gly Asp
770 775 780

Ile Pro Thr Ile Asn Tyr Lys Ala Ala Ser Ser Asp Leu Lys Ile Tyr
785 790 795 800

50 Ile Ser Pro Lys Leu Arg Ile Ile His Asn Gly Tyr Glu Gly Gln Lys
805 810 815

55 Arg Asn Gln Cys Asn Leu Met Asn Lys Tyr Gly Lys Leu Gly Asp Lys
820 825 830

Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn
835 840 845

60

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

65 (A) LENGTH: 16 amino acids
(B) TYPE: amino acid

(C) STRANDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULAR TYPE: protein
(v) FRAGMENT TYPE: N-terminal

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Arg Tyr Tyr Asn Leu Ser Asp Glu Glu Leu Ser Gln Phe Ile Gly
1 5 10 15

15 Lys

(2) INFORMATION FOR SEQ ID NO:39:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULAR TYPE: protein
(v) FRAGMENT TYPE: N-terminal

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Thr Ala Thr Asp Val Ser Gly Pro Val Glu Ile Asn Thr Ala
1 5 10 15

35 Ile Ser Pro Ala Lys
20

40 (2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDNESS: single
45 (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein
(v) FRAGMENT TYPE: N-terminal
50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

55 Ala Asn Ser Leu Tyr Ala Leu Phe Leu Pro Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:41:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids

(B) TYPE: amino acid
(C) STRANDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: N-terminal

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Leu Arg Ser Ala Asn Thr Leu Thr Asp Leu Phe Leu Pro Gln
1 5 10

15 (2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULAR TYPE: protein

25 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

30 Arg Ala Leu Glu Val Glu Arg Thr Val Ser Leu Ala Glu Val Tyr
1 5 10 15
Ala Gly Leu Glu

35

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULAR TYPE: protein

45

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

50

Ile Arg Glu Asp Tyr Pro Ala Ser Leu Gly Lys
1 5 10

55 (2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDNESS: single
(D) TOPOLOGY: linear

60

(ii) MOLECULAR TYPE: protein

5 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

10 Asp Asp Ser Gly Asp Asp Asp Lys Val Thr Asn Thr Asp Ile His
1 5 10 15
Arg

15 (2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
20 (C) STRANDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

25 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

30 Asp Val Xaa Gly Ser Glu Lys Ala Asn Glu Lys Leu Lys
1 5 10

35 (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7551 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46 (ccdA):

45 ATG AAC GAG TCT GTA AAA GAG ATA CCT GAT GTA TTA AAA AGC CAG TGT 48
Met Asn Glu Ser Val Lys Glu Ile Pro Asp Val Leu Lys Ser Gln Cys
1 5 10 15

50 GGT TTT AAT TGT CTG ACA GAT ATT AGC CAC AGC TCT TTT AAT GAA TTT 96
Gly Phe Asn Cys Leu Thr Asp Ile Ser His Ser Ser Phe Asn Glu Phe
20 25 30

55 CGC CAG CAA GTA TCT GAG CAC CTC TCC TGG TCC GAA ACA CAC GAC TTA 144
Arg Gln Gln Val Ser Glu His Leu Ser Trp Ser Glu Thr His Asp Leu
35 40 45

60 TAT CAT GAT GCA CAA CAG GCA CAA AAG GAT AAT CGC CTG TAT GAA GCG 192
Tyr His Asp Ala Gln Gln Ala Gln Lys Asp Asn Arg Leu Tyr Glu Ala
50 55 60

65 CGT ATT CTC AAA CGC GCC AAT CCC CAA TTA CAA AAT GCG GTG CAT CTT 240
Arg Ile Leu Lys Arg Ala Asn Pro Gln Leu Gln Asn Ala Val His Leu
65 70 75 80

	GCC ATT CTC GCT CCC AAT GCT GAA CTG ATA GGC TAT AAC AAT GAA TTT	288
	Ala Ile Leu Ala Pro Asn Ala Glu Leu Ile Gly Tyr Asn Asn Gln Phe	
	85 30 95	
5	AGC GGT AGA GCC AGT CAA TAT GTT CCG CCG GGT ACC GTT TCT TCC ATG	336
	Ser Gly Arg Ala Ser Gln Tyr Val Ala Pro Gly Thr Val Ser Ser Met	
	100 105 110	
10	TTC TCC CCC GCC GCT TAT TTG ACT GAA CTT TAT CGT GAA GCA CCG AAT	384
	Phe Ser Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Arg Asn	
	115 120 125	
15	TTA CAC GCA AGT GAC TCC GTT TAT TAT CTG GAT ACC CCG CCG CCA GAT	432
	Leu His Ala Ser Asp Ser Val Tyr Tyr Leu Asp Thr Arg Arg Pro Asp	
	130 135 140	
20	CTC AAA TCA ATG GCG CTC AGT CAG CAA AAT ATG GAT ATA GAA TTA TCC	480
	Leu Lys Ser Met Ala Leu Ser Gln Gln Asn Met Asp Ile Glu Leu Ser	
	145 150 155 160	
	ACA CTC TCT TTG TCC AAT GAG CTG TTA TTG GAA AGC ATT AAA ACT GAA	528
	Thr Leu Ser Leu Ser Asn Glu Leu Leu Leu Glu Ser Ile Lys Thr Glu	
	165 170 175	
25	TCT AAA CTG GAA AAC TAT ACT AAA GTG ATG GAA ATG CTC TCC ACT TTC	576
	Ser Lys Leu Glu Asn Tyr Thr Lys Val Met Glu Met Leu Ser Thr Phe	
	180 185 190	
30	CGT CCT TCC GGC GCA ACG CCT TAT CAT GAT GCT TAT GAA AAT GTG CGT	624
	Arg Pro Ser Gly Ala Thr Pro Tyr His Asp Ala Tyr Glu Asn Val Arg	
	195 200 205	
35	GAA GTT ATC CAG CTA CAA GAT CCT GGA CTT GAG CAA CTC AAT GCA TCA	672
	Glu Val Ile Gln Leu Gln Asp Pro Gly Leu Glu Gln Leu Asn Ala Ser	
	210 215 220	
40	CCG GCA ATT GCC GGG TTG ATG CAT CAA GCC TCC CTA TTG GGT ATT AAC	720
	Pro Ala Ile Ala Gly Leu Met His Gln Ala Ser Leu Leu Gly Ile Asn	
	225 230 235 240	
	GCT TCA ATC TCG CCT GAG CTA TTT AAT ATT CTG ACG GAG GAG ATT ACC	768
	Ala Ser Ile Ser Pro Glu Leu Phe Asn Ile Leu Thr Glu Glu Ile Thr	
	245 250 255	
45	GAA GGT AAT GCT GAG GAA CTT TAT AAG AAA AAT TTT GGT AAT ATC GAA	816
	Glu Gly Asn Ala Glu Glu Leu Tyr Lys Lys Asn Phe Gly Asn Ile Glu	
	260 265 270	
50	CCG GCC TCA TTG GCT ATG CCG GAA TAC CTT AAA CGT TAT TAT AAT TTA	864
	Pro Ala Ser Leu Ala Met Pro Glu Tyr Leu Lys Arg Tyr Tyr Asn Leu	
	275 280 285	
55	AGC GAT GAA GAA CTT AGT CAG TTT ATT GGT AAA GCC AGC AAT TTT GGT	912
	Ser Asp Glu Glu Leu Ser Gln Phe Ile Gly Lys Ala Ser Asn Phe Gly	
	290 295 300	
60	CAA CAG GAA TAT AGT AAT AAC CAA CTT ATT ACT CCG GTA GTC AAC AGC	960
	Gln Gln Glu Tyr Ser Asn Asn Gln Leu Ile Thr Pro Val Val Asn Ser	
	305 310 315 320	
	AGT GAT GGC ACG GTT AAG GTA TAT CGG ATC ACC CCG GAA TAT ACA ACC	1008
	Ser Asp Gly Thr Val Lys Val Tyr Arg Ile Thr Arg Glu Tyr Thr Thr	
	325 330 335	
65	AAT GCT TAT CAA ATG GAT GTG GAG CTA TTT CCC TTC GGT GGT GAG AAT	1056
	Asn Ala Tyr Gln Met Asp Val Glu Leu Phe Pro Phe Gly Gly Glu Asn	
	340 345 350	
70	TAT CCG TTA GAT TAT AAA TTC AAA AAT TTT TAT AAT GCC TCT TAT TTA	1104
	Tyr Arg Leu Asp Tyr Lys Phe Lys Asn Phe Tyr Asn Ala Ser Tyr Leu	
	355 360 365	

5	TCC ATC AAG TTA AAT GAT AAA AGA GAA CTT GTT CGA ACT GAA GGC GCT 1152
	Ser Ile Lys Leu Asn Asp Lys Arg Glu Leu Val Arg Thr Glu Gly Ala 370 375 380
10	CCT CAA GTC AAT ATA GAA TAC TCC GCA AAT ATC ACA TTA AAT ACC GCT 1200
	Pro Gln Val Asn Ile Glu Tyr Ser Ala Asn Ile Thr Leu Asn Thr Ala 385 390 395 400
15	GAT ATC AGT CAA CCT TTT GAA ATT GGC CTG ACA CGA GTA CTT CCT TCC 1248
	Asp Ile Ser Gln Pro Phe Glu Ile Gly Leu Thr Arg Val Leu Pro Ser 405 410 415
20	GGT TCT TGG GCA TAT GCC GCC GCA AAA TTT ACC GTT GAA GAG TAT AAC 1296
	Gly Ser Trp Ala Tyr Ala Ala Lys Phe Thr Val Glu Glu Tyr Asn 420 425 430
25	CAA TAC TCT TTT CTG CTA AAA CTT AAC AAG GCT ATT CGT CTA TCA CGT 1344
	Gln Tyr Ser Phe Leu Leu Lys Leu Asn Lys Ala Ile Arg Leu Ser Arg 435 440 445
30	GCG ACA GAA TTG TCA CCC ACG ATT CTG GAA GGC ATT GTG CGC AGT GTT 1392
	Ala Thr Glu Leu Ser Pro Thr Ile Leu Glu Gly Ile Val Arg Ser Val 450 455 460
35	AAT CTA CAA CTG GAT ATC AAC ACA GAC GTA TTA CGT AAA GTT TTT CTG 1440
	Asn Leu Gln Leu Asp Ile Asn Thr Asp Val Leu Gly Lys Val Phe Leu 465 470 475 480
40	ACT AAA TAT TAT ATG CAG CGT TAT GCT ATT CAT GCT GAA ACT GCC CTG 1488
	Thr Lys Tyr Tyr Met Gln Arg Tyr Ala Ile His Ala Glu Thr Ala Leu 485 490 495
45	ATA CTA TGC AAC GCG CCT ATT TCA CAA CGT TCA TAT GAT AAT CAA CCT 1536
	Ile Leu Cys Asn Ala Pro Ile Ser Gln Arg Ser Tyr Asp Asn Gln Pro 500 505 510
50	AGC CAA TTT GAT CGC CTG TTT AAT ACG CCA TTA CTG AAC GGA CAA TAT 1584
	Ser Gln Phe Asp Arg Leu Phe Asn Thr Pro Leu Leu Asn Gly Gln Tyr 515 520 525
55	TTT TCT ACC GGC GAT GAG GAG ATT GAT TTA AAT TCA GGT AGC ACC GGC 1632
	Phe Ser Thr Gly Asp Glu Glu Ile Asp Leu Asn Ser Gly Ser Thr Gly 530 535 540
60	GAT TGG CGA AAA ACC ATA CTT AAG CGT GCA TTT AAT ATT GAT GAT GTC 1680
	Asp Trp Arg Lys Thr Ile Leu Lys Arg Ala Phe Asn Ile Asp Asp Val 545 550 555 560
65	TCG CTC TTC CGC CTG CTT AAA ATT ACC GAC CAT GAT AAT AAA GAT GGA 1728
	Ser Leu Phe Arg Leu Leu Lys Ile Thr Asp His Asp Asn Lys Asp Gly 565 570 575
70	AAA ATT AAA AAT AAC CTA AAG AAT CTT TCC AAT TTA TAT ATT GGA AAA 1776
	Lys Ile Lys Asn Asn Leu Lys Asn Leu Ser Asn Leu Tyr Ile Gly Lys 580 585 590
75	TTA CTG GCA GAT ATT CAT CAA TTA ACC ATT GAT GAA CTG GAT TTA TTA 1824
	Leu Leu Ala Asp Ile His Gln Leu Thr Ile Asp Glu Leu Asp Leu Leu 595 600 605
80	CTG ATT GCC GTA GGT GAA GGA AAA ACT AAT TTA TCC GCT ATC AGT GAT 1872
	Leu Ile Ala Val Gly Glu Gly Lys Thr Asn Leu Ser Ala Ile Ser Asp 610 615 620
85	AAG CAA TTG GCT ACC CTG ATC AGA AAA CTC AAT ACT ATT ACC AGC TGG 1920
	Lys Gln Leu Ala Thr Leu Ile Arg Lys Leu Asn Thr Ile Thr Ser Trp 625 630 635 640
90	CTA CAT ACA CAG AAG TGG AGT GTA TTC CAG CTA TTT ATC ATC ACC TCC 1968
	Leu His Thr Gln Lys Trp Ser Val Phe Gln Leu Phe Ile Met Thr Ser 645 650 655

	545	650	655	
5	ACC AGC TAT AAC AAA ACG CTA ACG CCT GAA ATT AAG AAT TTG CTG GAT Thr Ser Tyr Asn Lys Thr Leu Thr Pro Glu Ile Lys Asn Leu Leu Asp 660 665 670	2016		
10	ACC GTC TAC CAC GGT TTA CAA GGT TTT GAT AAA GAC AAA GCA GAT TTG Thr Val Tyr His Gly Leu Gln Gly Phe Asp Lys Asp Lys Ala Asp Leu 675 680 685	2064		
	CTA CAT GTC ATG GCG CCC TAT ATT GCG GCC ACC TTG CAA TTA TCA TCG Leu His Val Met Ala Pro Tyr Ile Ala Ala Thr Leu Gln Leu Ser Ser 690 695 700	2112		
15	GAA AAT GTC GCC CAC TCG GTA CTC CTT TGG GCA GAT AAG TTA CAG CCC Glu Asn Val Ala His Ser Val Leu Leu Trp Ala Asp Lys Leu Gln Pro 705 710 715 720	2160		
20	GGC GAC GGC GCA ATG ACA GCA GAA AAA TTC TGG GAC TCG TTG AAT ACT Gly Asp Gly Ala Met Thr Ala Glu Lys Phe Trp Asp Trp Leu Asn Thr 725 730 735	2208		
25	AAG TAT ACG CCG GGT TCA TCG GAA GCC GTA GAA ACG CAG GAA CAT ATC Lys Tyr Thr Pro Gly Ser Ser Glu Ala Val Glu Thr Gln Glu His Ile 740 745 750	2256		
30	GTT CAG TAT TGT CAG GCT CTG GCA CAA TTG GAA ATG GTT TAC CAT TCC Val Gln Tyr Cys Gln Ala Leu Ala Gln Leu Glu Met Val Tyr His Ser 755 760 765	2304		
	ACC GGC ATC AAC GAA AAC GCC TTC CGT CTA TTT GTG ACA AAA CCA GAG Thr Gly Ile Asn Glu Asn Ala Phe Arg Leu Phe Val Thr Lys Pro Glu 770 775 780	2352		
35	ATG TTT GGC GCT GCA ACT GGA GCA GCG CCC GCG CAT GAT GCC CTT TCA Met Phe Gly Ala Ala Thr Gly Ala Ala Pro Ala His Asp Ala Leu Ser 785 790 795 800	2400		
40	CTG ATT ATG CTG ACA CGT TTT GCG GAT TGG GTG AAC GCA CTA GGC GAA Leu Ile Met Leu Thr Arg Phe Ala Asp Trp Val Asn Ala Leu Gly Glu 805 810 815	2448		
45	AAA GCG TCC TCG GTG CTA GCG GCA TTT GAA GCT AAC TCG TTA ACG GCA Lys Ala Ser Ser Val Leu Ala Ala Phe Glu Ala Asn Ser Leu Thr Ala 820 825 830	2496		
50	GAA CAA CTG GCT GAT GCC ATG AAT CTT GAT GCT AAT TTG CTG TTG CAA Glu Gln Leu Ala Asp Ala Met Asn Leu Asp Ala Asn Leu Leu Leu Gln 835 840 845	2544		
	GCC AGT ATT CAA GCA CAA AAT CAT CAA CAT CTT CCC CCA GTA ACT CCA Ala Ser Ile Gln Ala Gln Asn His Gln His Leu Pro Pro Val Thr Pro 850 855 860	2592		
55	GAA AAT GCG TTC TCC TGT TGG ACA TCT ATC AAT ACT ATC CTG CAA TGG Glu Asn Ala Phe Ser Cys Trp Thr Ser Ile Asn Thr Ile Leu Gln Trp 865 870 875 880	2640		
60	GTT AAT GTC GCA CAA CAA TTG AAT GTC GCC CCA CAG GGC GTT TCC GCT Val Asn Val Ala Gln Gln Leu Asn Val Ala Pro Gln Gly Val Ser Ala 885 890 895	2688		
65	TTG GTC GGG CTG GAT TAT ATT CAA TCA ATG AAA GAG ACA CCG ACC TAT Leu Val Gly Leu Asp Tyr Ile Gln Ser Met Lys Glu Thr Pro Thr Tyr 900 905 910	2736		
70	GCC CAG TGG GAA AAC GCG GCA GGC GTA TTA ACC GCC GCG TTG AAT TCA Ala Gln Trp Glu Asn Ala Ala Gly Val Leu Thr Ala Gly Leu Asn Ser 915 920 925	2784		
	CAA CAG CCT AAT ACA TTA CAC GCT TTT CTG GAT GAA TCT CGC AGT GCC	2832		

	Gln Gln Ala Asn Thr Leu His Ala Phe Leu Asp Glu Ser Arg Ser Ala	
	930 935 940	
5	GCA TTA AGC ACC TAC TAT ATC CGT CAA GTC GCC AAG GCA GCG GCG GCT Ala Leu Ser Thr Tyr Tyr Ile Arg Gln Val Ala Lys Ala Ala Ala Ala	2880
	945 950 955 960	
10	ATT AAA AGC CGT GAT GAC TTG TAT CAA TAC TTA CTG ATT GAT AAT CAG Ile Lys Ser Arg Asp Asp Leu Tyr Gln Tyr Leu Leu Ile Asp Asn Gln	2928
	965 970 975	
15	GTT TCT GCG GCA ATA AAA ACC ACC CGG ATC GCC GAA GCC ATT GCC AGT Val Ser Ala Ala Ile Lys Thr Thr Arg Ile Ala Glu Ala Ile Ala Ser	2976
	980 985 990	
	ATT CAA CTG TAC GTC AAC CGG GCA TTG GAA AAT GTG GAA GAA AAT GCC Ile Gln Leu Tyr Val Asn Arg Ala Leu Glu Asn Val Glu Glu Asn Ala	3024
	995 1000 1005	
20	AAT TCG GGG GTT ATC AGC CGC CAA TTC TTT ATC GAC TGG GAC AAA TAC Asn Ser Gly Val Ile Ser Arg Gln Phe Phe Ile Asp Trp Asp Lys Tyr	3072
	1010 1015 1020	
25	AAT AAA CGC TAC AGC ACT TGG GCG GGT GTT TCT CAA TTA GTT TAC TAC Asn Lys Arg Tyr Ser Thr Trp Ala Gly Val Ser Gln Leu Val Tyr Tyr	3120
	1025 1030 1035 1040	
30	CCG GAA AAC TAT ATT GAT CCG ACC ATG CGT ATC GGA CAA ACC AAA ATG Pro Glu Asn Tyr Ile Asp Pro Thr Met Arg Ile Gly Gln Thr Lys Met	3168
	1045 1050 1055	
35	ATG GAC GCA TTA CTG CAA TCC GTC AGC CAA AGC CAA TTA AAC GCC GAT Met Asp Ala Leu Leu Gln Ser Val Ser Gln Ser Gln Leu Asn Ala Asp	3216
	1060 1065 1070	
	ACC GTC GAA GAT GCC TTT ATG TCT TAT CTG ACA TCG TTT GAA CAA GTG Thr Val Glu Asp Ala Phe Met Ser Tyr Leu Thr Ser Phe Glu Gln Val	3264
	1075 1080 1085	
40	GCT AAT CTT AAA GTT ATT AGC CCA TAT CAC GAT AAT ATT AAT AAC GAT Ala Asn Leu Lys Val Ile Ser Ala Tyr His Asp Asn Ile Asn Asn Asp	3312
	1090 1095 1100	
45	CAA GGG CTG ACC TAT TTT ATC GGA CTC AGT GAA ACT GAT GCC GGT GAA Gln Gly Leu Thr Tyr Phe Ile Gly Leu Ser Glu Thr Asp Ala Gly Glu	3360
	1105 1110 1115 1120	
50	TAT TAT TGG CGC AGT GTC GAT CAC AGT AAA TTC AAC GAC GGT AAA TTC Tyr Tyr Trp Arg Ser Val Asp His Ser Lys Phe Asn Asp Gly Lys Phe	3408
	1125 1130 1135	
55	GCG GCT AAT GCC TGG AGT GAA TGG CAT AAA ATT GAT TGT CCA ATT AAC Ala Ala Asn Ala Trp Ser Glu Trp His Lys Ile Asp Cys Pro Ile Asn	3456
	1140 1145 1150	
	CCT TAT AAA AGC ACT ATC CGT CCA GTG ATA TAT AAA TCC CGC CTG TAT Pro Tyr Lys Ser Thr Ile Arg Pro Val Ile Tyr Lys Ser Arg Leu Tyr	3504
	1155 1160 1165	
60	CTG CTC TGG TTG GAA CAA AAG GAG ATC ACC AAA CAG ACA GGA AAT AGT Leu Leu Trp Leu Glu Gln Lys Glu Ile Thr Lys Gln Thr Gly Asn Ser	3552
	1170 1175 1180	
65	AAA GAT GGC TAT CAA ACT GAA ACG GAT TAT CGT TAT GAA CTA AAA TTG Lys Asp Gly Tyr Gln Thr Glu Thr Asp Tyr Arg Tyr Glu Leu Lys Leu	3600
	1185 1190 1195 1200	
70	GCG CAT ATC CGC TAT GAT GGC ACT TGG AAT ACG CCA ATC ACC TTT GAT Ala His Ile Arg Tyr Asp Gly Thr Trp Asn Thr Pro Ile Thr Phe Asp	3648
	1205 1210 1215	

	GTC AAT AAA AAA ATA TCC GAG CTA AAA CTG GAA AAA AAT AGA GCG CCC	3636
	Val Asn Lys Lys Ile Ser Glu Leu Lys Leu Glu Lys Asn Arg Ala Pro	
	1220 1225 1230	
5	GGA CTC TAT TGT GCC GGT TAT CAA GGT GAA GAT ACG TTG CTG GTG ATG	3744
	Gly Leu Tyr Cys Ala Gly Tyr Gln Gly Glu Asp Thr Leu Leu Val Met	
	1235 1240 1245	
10	TTT TAT AAC CAA CAA GAC ACA CTA GAT AGT TAT AAA AAC GCT TCA ATG	3792
	Phe Tyr Asn Gln Gln Asp Thr Leu Asp Ser Tyr Lys Asn Ala Ser Met	
	1250 1255 1260	
15	CAA GGA CTA TAT ATC TTT GCT GAT ATG GCA TCC AAA GAT ATG ACC CCA	3840
	Gln Gly Leu Tyr Ile Phe Ala Asp Met Ala Ser Lys Asp Met Thr Pro	
	1265 1270 1275 1280	
20	GAA CAG AGC AAT GTT TAT CGG GAT AAT AGC TAT CAA CAA TTT GAT ACC	3888
	Glu Gln Ser Asn Val Tyr Arg Asp Asn Ser Tyr Gln Gln Phe Asp Thr	
	1285 1290 1295	
25	AAT AAT GTC AGA AGA GTG AAT AAC CGC TAT GCA GAG GAT TAT GAG ATT	3936
	Asn Asn Val Arg Arg Val Asn Asn Arg Tyr Ala Glu Asp Tyr Glu Ile	
	1300 1305 1310	
30	CCT TCC TCG GTA AGT AGC CGT AAA GAC TAT GGT TGG GGA GAT TAT TAC	3984
	Pro Ser Ser Val Ser Ser Arg Lys Asp Tyr Gly Trp Gly Asp Tyr Tyr	
	1315 1320 1325	
35	CTC AGC ATG GTA TAT AAC GGA GAT ATT CCA ACT ATC AAT TAC AAA GCC	4032
	Leu Ser Met Val Tyr Asn Gly Asp Ile Pro Thr Ile Asn Tyr Lys Ala	
	1330 1335 1340	
40	GCA TCA AGT GAT TTA AAA ATC TAT ATC TCA CCA AAA TTA AGA ATT ATT	4080
	Ala Ser Ser Asp Leu Lys Ile Tyr Ile Ser Pro Lys Leu Arg Ile Ile	
	1345 1350 1355 1360	
45	CAT AAT GGA TAT GAA GGA CAG AAG CGC AAT CAA TGC AAT CTG ATG AAT	4128
	His Asn Gly Tyr Glu Gly Gln Lys Arg Asn Gln Cys Asn Leu Met Asn	
	1365 1370 1375	
50	AAA TAT GGC AAA CTA GGT GAT AAA TTT ATT GTT TAT ACT AGC TTG GGG	4176
	Lys Tyr Gly Lys Leu Gly Asp Lys Phe Ile Val Tyr Thr Ser Leu Gly	
	1380 1385 1390	
55	GTC AAT CCA AAT AAC TCG TCA AAT AAG CTC ATG TTT TAC CCC GTC TAT	4224
	Val Asn Pro Asn Asn Ser Ser Asn Lys Leu Met Phe Tyr Pro Val Tyr	
	1395 1400 1405	
60	CAA TAT AGC GGA AAC ACC AGT GGA CTC AAT CAA GGG AGA CTA CTA TTC	4272
	Gln Tyr Ser Gly Asn Thr Ser Gly Leu Asn Gln Gly Arg Leu Leu Phe	
	1410 1415 1420	
65	CAC CGT GAC ACC ACT TAT CCA TCT AAA GTA GAA GCT TGG ATT CCT GGA	4320
	His Arg Asp Thr Thr Tyr Pro Ser Lys Val Glu Ala Trp Ile Pro Gly	
	1425 1430 1435 1440	
70	GCA AAA CGT TCT CTA ACC AAC CAA AAT GCC GCC ATT GGT GAT GAT TAT	4368
	Ala Lys Arg Ser Leu Thr Asn Gln Asn Ala Ala Ile Gly Asp Asp Tyr	
	1445 1450 1455	
75	GCT ACA GAC TCT CTG AAT AAA CCG GAT GAT CTT AAG CAA TAT ATC TTT	4416
	Ala Thr Asp Ser Leu Asn Lys Pro Asp Asp Leu Lys Gln Tyr Ile Phe	
	1460 1465 1470	
80	ATG ACT GAC AGT AAA GGG ACT GCT ACT GAT GTC TCA GGC CCA GTA GAG	4464
	Met Thr Asp Ser Lys Gly Thr Ala Thr Asp Val Ser Gly Pro Val Glu	
	1475 1480 1485	
85	ATT AAT ACT GCA ATT TCT CCA GCA AAA GTT CAG ATA ATA GTC AAA GCG	4512
	Ile Asn Thr Ala Ile Ser Pro Ala Lys Val Gln Ile Ile Val Lys Ala	
	1490 1495 1500	

5	GCT GGC AAG GAG CAA ACT TTT ACC GCA GAT AAA GAT GTC TCC ATT CAG 4560 Gly Gly Lys Glu Gln Thr Phe Thr Ala Asp Lys Asp Val Ser Ile Gln 1505 1510 1515 1520
	CCA TCA CCT AGC TTT GAT GAA ATG AAT TAT CAA TTT AAT GCC CTT GAA 4608 Pro Ser Pro Ser Phe Asp Glu Met Asn Tyr Gln Phe Asn Ala Leu Glu 1525 1530 1535
10	ATA GAC GGT TCT GGT CTG AAT TTT ATT AAC AAC TCA GCC AGT ATT GAT 4656 Ile Asp Gly Ser Gly Leu Asn Phe Ile Asn Asn Ser Ala Ser Ile Asp 1540 1545 1550
15	GTT ACT TTT ACC GCA TTT GCG GAG GAT GGC CGC AAA CTG GGT TAT GAA 4704 Val Thr Phe Thr Ala Phe Ala Glu Asp Gly Arg Lys Leu Gly Tyr Glu 1555 1560 1565
20	AGT TTC AGT ATT CCT GTT ACC CTC AAG GTA AGT ACC GAT AAT GCC CTG 4752 Ser Phe Ser Ile Pro Val Thr Leu Lys Val Ser Thr Asp Asn Ala Leu 1570 1575 1580
25	ACC CTG CAC CAT AAT GAA AAT GGT GCG CAA TAT ATG CAA TGG CAA TCC 4800 Thr Leu His His Asn Glu Asn Gly Ala Gln Tyr Met Gln Trp Gln Ser 1585 1590 1595 1600
	TAT CGT ACC CGC CTG AAT ACT CTA TTT GCC CGC CAG TTG GTT GCA CGC 4848 Tyr Arg Thr Arg Leu Asn Thr Leu Phe Ala Arg Gln Leu Val Ala Arg 1605 1610 1615
30	GCC ACC ACC GGA ATC GAT ACA ATT CTG AGT ATG GAA ACT CAG AAT ATT 4896 Ala Thr Thr Gly Ile Asp Thr Ile Leu Ser Met Glu Thr Gln Asn Ile 1620 1625 1630
35	CAG GAA CCG CAG TTA GGC AAA GGT TTC TAT GCT ACG TTC GTG ATA CCT 4944 Gln Glu Pro Gln Leu Gly Lys Gly Phe Tyr Ala Thr Phe Val Ile Pro 1635 1640 1645
40	CCC TAT AAC CTA TCA ACT CAT GGT GAT GAA CGT TGG TTT AAG CTT TAT 4992 Pro Tyr Asn Leu Ser Thr His Gly Asp Glu Arg Trp Phe Lys Leu Tyr 1650 1655 1660
45	ATC AAA CAT GTT GTT GAT AAT AAT TCA CAT ATT ATC TAT TCA GGC CAG 5040 Ile Lys His Val Val Asp Asn Asn Ser His Ile Ile Tyr Ser Gly Gln 1665 1670 1675 1680
	CTA ACA GAT ACA AAT ATA AAC ATC ACA TTA TTT ATT CCT CTT GAT GAT 5088 Leu Thr Asp Thr Asn Ile Asn Ile Thr Leu Phe Ile Pro Leu Asp Asp 1685 1690 1695
50	GTC CCA TTG AAT CAA GAT TAT CAC GCC AAG GTT TAT ATG ACC TTC AAG 5136 Val Pro Leu Asn Gln Asp Tyr His Ala Lys Val Tyr Met Thr Phe Lys 1700 1705 1710
55	AAA TCA CCA TCA GAT GGT ACC TGG TGG GGC CCT CAC TTT GTT AGA GAT 5184 Lys Ser Pro Ser Asp Gly Thr Trp Trp Gly Pro His Phe Val Arg Asp 1715 1720 1725
60	GAT AAA GGA ATA GTA ACA ATA AAC CCT AAA TCC ATT TTG ACC CAT TTT 5232 Asp Lys Gly Ile Val Thr Ile Asn Pro Lys Ser Ile Leu Thr His Phe 1730 1735 1740
65	GAG AGC GTC AAT GTC CTG AAT AAT ATT AGT AGC GAA CCA ATG GAT TTC 5280 Glu Ser Val Asn Val Leu Asn Asn Ile Ser Ser Glu Pro Met Asp Phe 1745 1750 1755 1760
	AGC GGC GCT AAC AGC CTC TAT TTC TGG GAA CTG TTC TAC TAT ACC CCG 5328 Ser Gly Ala Asn Ser Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro 1765 1770 1775
70	ATG CTG GTT GCT CAA CGT TTG CTG CAT GAA CAG AAC TTC GAT GAA GCC 5376 Met Leu Val Ala Gln Arg Leu Leu His Glu Gln Asn Phe Asp Glu Ala

	1730	1785	1790	
5	AAC CGT TGG CTG AAA TAT GTC TGG AGT CCA TCC GGT TAT ATT GTC CAC Asn Arg Trp Leu Lys Tyr Val Trp Ser Pro Ser Gly Tyr Ile Val His 1795 1800 1805	5424		
10	GGC CAG ATT CAG AAC TAC CAG TGG AAC GTC CGC CCG TTA CTG GAA GAC Gly Gln Ile Gln Asn Tyr Gln Trp Asn Val Arg Pro Leu Leu Glu Asp 1810 1815 1820	5472		
15	ACC AGT TGG AAC AGT GAT CCT TTG GAT TCC GTC GAT CCT GAC GCG GTA Thr Ser Trp Asn Ser Asp Pro Leu Asp Ser Val Asp Pro Asp Ala Val 1825 1830 1835 1840	5520		
20	GCA CAG CAC GAT CCA ATG CAC TAC AAA GTT TCA ACT TTT ATG CGT ACC Ala Gln His Asp Pro Met His Tyr Lys Val Ser Thr Phe Met Arg Thr 1845 1850 1855	5568		
25	TTG GAT CTA TTG ATA GCA CGC GGC GAC CAT GCT TAT CGC CAA CTG GAA Leu Asp Leu Leu Ile Ala Arg Gly Asp His Ala Tyr Arg Gln Leu Glu 1860 1865 1870	5616		
30	CGA GAT ACA CTC AAC GAA GCG AAG ATG TGG TAT ATG CAA GCG CTG CAT Arg Asp Thr Leu Asn Glu Ala Lys Met Trp Tyr Met Gln Ala Leu His 1875 1880 1885	5664		
35	CTA TTA GGT GAC AAA CCT TAT CTA CCG CTG AGT ACG ACA TGG AGT GAT Leu Leu Gly Asp Lys Pro Tyr Leu Pro Leu Ser Thr Thr Trp Ser Asp 1890 1895 1900	5712		
40	CCA CGA CTA GAC AGA GCC GCG GAT ATC ACT ACC CAA AAT GCT CAC GAC Pro Arg Leu Asp Arg Ala Ala Asp Ile Thr Thr Gln Asn Ala His Asp 1905 1910 1915 1920	5760		
45	AGC GCA ATA GTC GCT CTG CCG CAG AAT ATA CCT ACA CCG GCA CCT TTA Ser Ala Ile Val Ala Leu Arg Gln Asn Ile Pro Thr Pro Ala Pro Leu 1925 1930 1935	5808		
50	TCA TTG CGC AGC GCT AAT ACC CTG ACT GAT CTC TTC CTG CCG CAA ATC Ser Leu Arg Ser Ala Asn Thr Leu Thr Asp Leu Phe Leu Pro Gln Ile 1940 1945 1950	5856		
55	AAT GAA GTG ATG ATG AAT TAC TGG CAG ACA TTA GCT CAG AGA GTA TAC Asn Glu Val Met Met Asn Tyr Trp Gln Thr Leu Ala Gln Arg Val Tyr 1955 1960 1965	5904		
60	AAT CTG CGT CAT AAC CTC TCT ATC GAC GGC CAG CCG TTA TAT CTG CCA Asn Leu Arg His Asn Leu Ser Ile Asp Gly Gln Pro Leu Tyr Leu Pro 1970 1975 1980	5952		
65	ATC TAT GCC ACA CCG GCC GAT CCG AAA GCG TTA CTC AGC GCC GCC GTT Ile Tyr Ala Thr Pro Ala Asp Pro Lys Ala Leu Leu Ser Ala Ala Val 1985 1990 1995 2000	6000		
70	GCC ACT TCT CAA GGT GGA GGC AAG CTA CCG GAA TCA TTT ATG TCC CTG Ala Thr Ser Gln Gly Gly Gly Lys Leu Pro Glu Ser Phe Met Ser Leu 2005 2010 2015	6048		
	TGG CGT TTC CCG CAC ATG CTG GAA AAT GCG CGC CGC ATG GTT AGC CAG Trp Arg Phe Pro His Met Leu Glu Asn Ala Arg Gly Met Val Ser Gln 2020 2025 2030	6096		
	CTC ACC CAG TTC GGC TCC ACG TTA CAA AAT ATT ATC GAA CGT CAG GAC Leu Thr Gln Phe Gly Ser Thr Leu Gln Asn Ile Ile Glu Arg Gln Asp 2035 2040 2045	6144		
	GCG GAA GCG CTC AAT GCG TTA TTA CAA AAT CAG GCC GCC GAG CTG ATA Ala Glu Ala Leu Asn Ala Leu Leu Gln Asn Gln Ala Ala Glu Leu Ile 2050 2055 2060	6192		
	TTG ACT AAC CTG AGC ATT CAG GAC AAA ACC ATT GAA GAA TTG GAT GCC	6240		

	Leu Thr Asn Leu Ser Ile Gln Asp Lys Thr Ile Glu Glu Leu Asp Ala	
	2055 2070 2075 2080	
5	GAG AAA ACG GTG TTG GAA AAA TCC AAA GCG GGA GCA CAA TCG CGC TTT Glu Lys Thr Val Leu Glu Lys Ser Lys Ala Gly Ala Gln Ser Arg Phe	6233
	2085 2090 2095	
10	GAT AGC TAC GGC AAA CTG TAC GAT GAG AAT ATC AAC GCC GGT GAA AAC Asp Ser Tyr Gly Lys Leu Tyr Asp Glu Asn Ile Asn Ala Gly Glu Asn	6336
	2100 2105 2110	
15	CAA GCC ATG ACG CTA CGA GCG TCC GCC GCC GGG CTT ACC ACG GCA GTT Gln Ala Met Thr Leu Arg Ala Ser Ala Ala Gly Leu Thr Thr Ala Val	6384
	2115 2120 2125	
	CAG GCA TCC CGT CTG GCC GGT GCG GCG GCT GAT CTG GTG CCT AAC ATC Gln Ala Ser Arg Leu Ala Gly Ala Ala Asp Leu Val Pro Asn Ile	6432
	2130 2135 2140	
20	TTC GGC TTT GCC GGT GGC GGC AGC CGT TGG GGG GCT ATC GCT GAG GCG Phe Gly Phe Ala Gly Gly Gly Ser Arg Trp Gly Ala Ile Ala Glu Ala	6480
	2145 2150 2155 2160	
25	ACA GGT TAT GTG ATG GAA TTC TCC GCG AAT GTT ATG AAC ACC GAA GCG Thr Gly Tyr Val Met Glu Phe Ser Ala Asn Val Met Asn Thr Glu Ala	6528
	2165 2170 2175	
30	GAT AAA ATT AGC CAA TCT GAA ACC TAC CGT CGT CGC CGT CAG GAG TGG Asp Lys Ile Ser Gln Ser Glu Thr Tyr Arg Arg Arg Arg Gln Glu Trp	6576
	2180 2185 2190	
35	GAG ATC CAG CGG AAT AAT GCC GAA GCG GAA TTG AAG CAA ATC GAT GCT Glu Ile Gln Arg Asn Asn Ala Glu Ala Glu Leu Lys Gln Ile Asp Ala	6624
	2195 2200 2205	
	CAG CTC AAA TCA CTC GCT GTA CGC CGC GAA GCC GCC GTA TTG CAG AAA Gln Leu Lys Ser Leu Ala Val Arg Arg Glu Ala Ala Val Leu Gln Lys	6672
	2210 2215 2220	
40	ACC AGT CTG AAA ACC CAA CAA GAA CAG ACC CAA TCT CAA TTG GCC TTC Thr Ser Leu Lys Thr Gln Gln Glu Gln Thr Gln Ser Gln Leu Ala Phe	6720
	2225 2230 2235 2240	
45	CTG CAA CGT AAG TTC AGC AAT CAG GCG TTA TAC AAC TGG CTG CGT GGT Leu Gln Arg Lys Phe Ser Asn Gln Ala Leu Tyr Asn Trp Leu Arg Gly	6768
	2245 2250 2255	
50	CGA CTG GCG GCG ATT TAC TTC CAG TTC TAC GAT TTG GCC GTC GCG CGT Arg Leu Ala Ala Ile Tyr Phe Gln Phe Tyr Asp Leu Ala Val Ala Arg	6816
	2260 2265 2270	
55	TGC CTG ATG GCA GAA CAA GCT TAC CGT TGG GAA CTC AAT GAT GAC TCT Cys Leu Met Ala Glu Gln Ala Tyr Arg Trp Glu Leu Asn Asp Asp Ser	6864
	2275 2280 2285	
	GCC CGC TTC ATT AAA CCG GGC GCC TGG CAG GGA ACC TAT GCC GGT CTG Ala Arg Phe Ile Lys Pro Gly Ala Trp Gln Gly Thr Tyr Ala Gly Leu	6912
	2290 2295 2300	
60	CTT GCA GGT GAA ACC TTG ATG CTG AGT CTG GCA CAA ATG GAA GAC GCT Leu Ala Gly Glu Thr Leu Met Leu Ser Leu Ala Gln Met Glu Asp Ala	6960
	2305 2310 2315 2320	
65	CAT CTG AAA CGC GAT AAA CGC GCA TTA GAG GTT GAA CGC ACA GTA TCG His Leu Lys Arg Asp Lys Arg Ala Leu Glu Val Glu Arg Thr Val Ser	7008
	2325 2330 2335	
70	CTG GCC GAA GTT TAT GCA GGA TTA CCA AAA GAT AAC GGT CCA TTT TCC Leu Ala Glu Val Tyr Ala Gly Leu Pro Lys Asp Asn Gly Pro Phe Ser	7056
	2340 2345 2350	

CTG GCT CAG GAA ATT GAC AAG CTG GTG AGT CAA GGT TCA GGC AGT GCC 7194
 Leu Ala Gln Glu Ile Asp Lys Leu Val Ser Gln Gly Ser Gly Ser Ala
 2355 2360 2365

5 GGC AGT GGT AAT AAT AAT TTG GCG TTC GGC GCC GGC ACG GAC ACT AAA 7152
 Gly Ser Gly Asn Asn Asn Leu Ala Phe Gly Ala Gly Thr Asp Thr Lys
 2370 2375 2380

10 ACC TCT TTG CAG GCA TCA GTT TCA TTC GCT GAT TTG AAA ATT CGT GAA 7200
 Thr Ser Leu Gln Ala Ser Val Ser Phe Ala Asp Leu Lys Ile Arg Glu
 2385 2390 2395 2400

15 GAT TAC CCG GCA TCG CTT GGC AAA ATT CGA CGT ATC AAA CAG ATC AGC 7248
 Asp Tyr Pro Ala Ser Leu Gly Lys Ile Arg Arg Ile Lys Gln Ile Ser
 2405 2410 2415

20 CTC ACT TTG CCC GCG CTA CTG GGA CCG TAT CAG GAT GTA CAG GCA ATA 7296
 Val Thr Leu Pro Ala Leu Leu Gly Pro Tyr Gln Asp Val Gln Ala Ile
 2420 2425 2430

TTG TCT TAC GGC GAT AAA GCC GGA TTA GCT AAC GGC TGT GAA GCG CTG 7344
 Leu Ser Tyr Gly Asp Lys Ala Gly Leu Ala Asn Gly Cys Glu Ala Leu
 2435 2440 2445

25 GCA GTT TCT CAC GGT ATG AAT GAC AGC GGC CAA TTC CAG CTC GAT TTC 7392
 Ala Val Ser His Gly Met Asn Asp Ser Gly Gln Phe Gln Leu Asp Phe
 2450 2455 2460

30 AAC GAT GGC AAA TTC CTG CCA TTC GAA GGC ATC GCC ATT GAT CAA GGC 7440
 Asn Asp Gly Lys Phe Leu Pro Phe Glu Gly Ile Ala Ile Asp Gln Gly
 2465 2470 2475 2480

35 ACG CTG ACA CTG AGC TTC CCA AAT GCA TCT ATG CCG GAG AAA GGT AAA 7488
 Thr Leu Thr Leu Ser Phe Pro Asn Ala Ser Met Pro Glu Lys Gly Lys
 2485 2490 2495

CAA GCC ACT ATG TTA AAA ACC CTG AAC GAT ATC ATT TTG CAT ATT CGC 7536
 Gln Ala Thr Met Leu Lys Thr Leu Asn Asp Ile Ile Leu His Ile Arg
 2500 2505 2510

40 TAC ACC ATT AAA TAA 7551
 Tyr Thr Ile Lys ...
 2516

45 (2) INFORMATION FOR SEQ ID NO:47:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2516 amino acids
 (B) TYPE: amino acids
 50 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47 (TcdA):

Features	From	To	Description
Peptide	1	2516	TcdA proteins
Peptide	89	1937	TcdA _{ii} peptide
Fragment	89	100	S2 N-terminus (SEQ ID NO:13)
Fragment	284	299	(SEQ ID NO:38)
Fragment	554	563	(SEQ ID NO:17)
Fragment	1080	1092	(SEQ ID NO:23; 12/13)
Fragment	1385	1400	(SEQ ID NO:18)
Fragment	1478	1497	(SEQ ID NO:39)
Fragment	1620	1642	(SEQ ID NO:21; 19/23)
Fragment	1938	1948	(SEQ ID NO:41)
Peptide	1938	2516	TcdA _{iii} peptide
Fragment	2327	2345	(SEQ ID NO:42)
Fragment	2398	2408	(SEQ ID NO:43)

60

65

Met Asn Glu Ser Val Lys Glu Ile Pro Asp Val Leu Lys Ser Gln Cys
 1 5 10 15
 5 Gly Phe Asn Cys Leu Thr Asp Ile Ser His Ser Ser Phe Asn Glu Phe
 20 25 30
 Arg Gln Gln Val Ser Glu His Leu Ser Trp Ser Glu Thr His Asp Leu
 35 40 45
 10 Tyr His Asp Ala Gln Gln Ala Gln Lys Asp Asn Arg Leu Tyr Glu Ala
 50 55 60
 Arg Ile Leu Lys Arg Ala Asn Pro Gln Leu Gln Asn Ala Val His Leu
 65 70 75 80
 Ala Ile Leu Ala Pro Asn Ala Glu Leu Ile Gly Tyr Asn Asn Gln Phe
 85 90 95
 20 Ser Gly Arg Ala Ser Gln Tyr Val Ala Pro Gly Thr Val Ser Ser Met
 100 105 110
 Phe Ser Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Arg Asn
 115 120 125
 25 Leu His Ala Ser Asp Ser Val Tyr Tyr Leu Asp Thr Arg Arg Pro Asp
 130 135 140
 Leu Lys Ser Met Ala Leu Ser Gln Gln Asn Met Asp Ile Glu Leu Ser
 145 150 155 160
 30 Thr Leu Ser Leu Ser Asn Glu Leu Leu Leu Glu Ser Ile Lys Thr Glu
 165 170 175
 Ser Lys Leu Glu Asn Tyr Thr Lys Val Met Glu Met Leu Ser Thr Phe
 180 185 190
 Arg Pro Ser Gly Ala Thr Pro Tyr His Asp Ala Tyr Glu Asn Val Arg
 195 200 205
 40 Glu Val Ile Gln Leu Gln Asp Pro Gly Leu Glu Gln Leu Asn Ala Ser
 210 215 220
 Pro Ala Ile Ala Gly Leu Met His Gln Ala Ser Leu Leu Gly Ile Asn
 225 230 235 240
 Ala Ser Ile Ser Pro Glu Leu Phe Asn Ile Leu Thr Glu Glu Ile Thr
 245 250 255
 50 Glu Gly Asn Ala Glu Glu Leu Tyr Lys Lys Asn Phe Gly Asn Ile Glu
 260 265 270
 Pro Ala Ser Leu Ala Met Pro Glu Tyr Leu Lys Arg Tyr Tyr Asn Leu
 275 280 285
 55 Ser Asp Glu Glu Leu Ser Gln Phe Ile Gly Lys Ala Ser Asn Phe Gly
 290 295 300
 Gln Gln Glu Tyr Ser Asn Asn Gln Leu Ile Thr Pro Val Val Asn Ser
 305 310 315 320
 Ser Asp Gly Thr Val Lys Val Tyr Arg Ile Thr Arg Glu Tyr Thr Thr
 325 330 335
 65 Asn Ala Tyr Gln Met Asp Val Glu Leu Phe Pro Phe Gly Gly Glu Asn
 340 345 350
 Tyr Arg Leu Asp Tyr Lys Phe Lys Asn Phe Tyr Asn Ala Ser Tyr Leu
 355 360 365
 70 Ser Ile Lys Leu Asn Asp Lys Arg Glu Leu Val Arg Thr Glu Gly Ala

	370	375	380
	Pro Gln Val Asn Ile Glu Tyr Ser Ala Asn Ile Thr Leu Asn Thr Ala		
	385	390	395 400
5	Asp Ile Ser Gln Pro Phe Glu Ile Gly Leu Thr Arg Val Leu Pro Ser		
		405 410	415
10	Gly Ser Trp Ala Tyr Ala Ala Ala Lys Phe Thr Val Glu Glu Tyr Asn		
		420 425	430
	Gln Tyr Ser Phe Leu Leu Lys Leu Asn Lys Ala Ile Arg Leu Ser Arg		
		435 440	445
15	Ala Thr Glu Leu Ser Pro Thr Ile Leu Glu Gly Ile Val Arg Ser Val		
		450 455	460
	Asn Leu Gln Leu Asp Ile Asn Thr Asp Val Leu Gly Lys Val Phe Leu		
		465 470	475 480
20	Thr Lys Tyr Tyr Met Gln Arg Tyr Ala Ile His Ala Glu Thr Ala Leu		
		485 490	495
	Ile Leu Cys Asn Ala Pro Ile Ser Gln Arg Ser Tyr Asp Asn Gln Pro		
		500 505	510
	Ser Gln Phe Asp Arg Leu Phe Asn Thr Pro Leu Leu Asn Gly Gln Tyr		
		515 520	525
30	Phe Ser Thr Gly Asp Glu Glu Ile Asp Leu Asn Ser Gly Ser Thr Gly		
		530 535	540
	Asp Trp Arg Lys Thr Ile Leu Lys Arg Ala Phe Asn Ile Asp Asp Val		
		545 550	555 560
35	Ser Leu Phe Arg Leu Leu Lys Ile Thr Asp His Asp Asn Lys Asp Gly		
		565 570	575
	Lys Ile Lys Asn Asn Leu Lys Asn Leu Ser Asn Leu Tyr Ile Gly Lys		
		580 585	590
40	Leu Leu Ala Asp Ile His Gln Leu Thr Ile Asp Glu Leu Asp Leu Leu		
		595 600	605
45	Leu Ile Ala Val Gly Glu Gly Lys Thr Asn Leu Ser Ala Ile Ser Asp		
		610 615	620
	Lys Gln Leu Ala Thr Leu Ile Arg Lys Leu Asn Thr Ile Thr Ser Trp		
		625 630	635 640
50	Leu His Thr Gln Lys Trp Ser Val Phe Gln Leu Phe Ile Met Thr Ser		
		645 650	655
	Thr Ser Tyr Asn Lys Thr Leu Thr Pro Glu Ile Lys Asn Leu Leu Asp		
		660 665	670
55	Thr Val Tyr His Gly Leu Gln Gly Phe Asp Lys Asp Lys Ala Asp Leu		
		675 680	685
60	Leu His Val Met Ala Pro Tyr Ile Ala Ala Thr Leu Gln Leu Ser Ser		
		690 695	700
	Glu Asn Val Ala His Ser Val Leu Leu Trp Ala Asp Lys Leu Gln Pro		
		705 710	715 720
65	Gly Asp Gly Ala Met Thr Ala Glu Lys Phe Trp Asp Trp Leu Asn Thr		
		725 730	735
70	Lys Tyr Thr Pro Gly Ser Ser Glu Ala Val Glu Thr Gln Glu His Ile		
		740 745	750

Val Gln Tyr Cys Gln Ala Leu Ala Gln Leu Glu Met Val Tyr His Ser
 755 760 765
 5 Thr Gly Ile Asn Glu Asn Ala Phe Arg Leu Phe Val Thr Lys Pro Glu
 770 775 780
 Met Phe Gly Ala Ala Thr Gly Ala Ala Pro Ala His Asp Ala Leu Ser
 785 790 795 800
 10 Leu Ile Met Leu Thr Arg Phe Ala Asp Trp Val Asn Ala Leu Gly Glu
 805 810 815
 Lys Ala Ser Ser Val Leu Ala Ala Phe Glu Ala Asn Ser Leu Thr Ala
 820 825 830
 15 Glu Gln Leu Ala Asp Ala Met Asn Leu Asp Ala Asn Leu Leu Leu Gln
 835 840 845
 20 Ala Ser Ile Gln Ala Gln Asn His Gln His Leu Pro Pro Val Thr Pro
 850 855 860
 Glu Asn Ala Phe Ser Cys Trp Thr Ser Ile Asn Thr Ile Leu Gln Trp
 865 870 875 880
 25 Val Asn Val Ala Gln Gln Leu Asn Val Ala Pro Gln Gly Val Ser Ala
 885 890 895
 Leu Val Gly Leu Asp Tyr Ile Gln Ser Met Lys Glu Thr Pro Thr Tyr
 900 905 910
 30 Ala Gln Trp Glu Asn Ala Ala Gly Val Leu Thr Ala Gly Leu Asn Ser
 915 920 925
 Gln Gln Ala Asn Thr Leu His Ala Phe Leu Asp Glu Ser Arg Ser Ala
 930 935 940
 35 Ala Leu Ser Thr Tyr Tyr Ile Arg Gln Val Ala Lys Ala Ala Ala Ala
 945 950 955 960
 40 Ile Lys Ser Arg Asp Asp Leu Tyr Gln Tyr Leu Leu Ile Asp Asn Gln
 965 970 975
 Val Ser Ala Ala Ile Lys Thr Thr Arg Ile Ala Glu Ala Ile Ala Ser
 980 985 990
 45 Ile Gln Leu Tyr Val Asn Arg Ala Leu Glu Asn Val Glu Glu Asn Ala
 995 1000 1005
 50 Asn Ser Gly Val Ile Ser Arg Gln Phe Phe Ile Asp Trp Asp Lys Tyr
 1010 1015 1020
 Asn Lys Arg Tyr Ser Thr Trp Ala Gly Val Ser Gln Leu Val Tyr Tyr
 1025 1030 1035 1040
 55 Pro Glu Asn Tyr Ile Asp Pro Thr Met Arg Ile Gly Gln Thr Lys Met
 1045 1050 1055
 Met Asp Ala Leu Leu Gln Ser Val Ser Gln Ser Gln Leu Asn Ala Asp
 1060 1065 1070
 60 Thr Val Glu Asp Ala Phe Met Ser Tyr Leu Thr Ser Phe Glu Gln Val
 1075 1080 1085
 Ala Asn Leu Lys Val Ile Ser Ala Tyr His Asp Asn Ile Asn Asn Asp
 1090 1095 1100
 65 Gln Gly Leu Thr Tyr Phe Ile Gly Leu Ser Glu Thr Asp Ala Gly Glu
 1105 1110 1115 1120
 70 Tyr Tyr Trp Arg Ser Val Asp His Ser Lys Phe Asn Asp Gly Lys Phe
 1125 1130 1135

Ala Ala Asn Ala Trp Ser Glu Trp His Lys Ile Asp Cys Pro Ile Asn
1140 1145 1150

5 Pro Tyr Lys Ser Thr Ile Arg Pro Val Ile Tyr Lys Ser Arg Leu Tyr
1155 1160 1165

Leu Leu Trp Leu Glu Gln Lys Glu Ile Thr Lys Gln Thr Gly Asn Ser
1170 1175 1180

10 Lys Asp Gly Tyr Gln Thr Glu Thr Asp Tyr Arg Tyr Glu Leu Lys Leu
1185 1190 1195 1200

Ala His Ile Arg Tyr Asp Gly Thr Trp Asn Thr Pro Ile Thr Phe Asp
1205 1210 1215

15 Val Asn Lys Lys Ile Ser Glu Leu Lys Leu Glu Lys Asn Arg Ala Pro
1220 1225 1230

20 Gly Leu Tyr Cys Ala Gly Tyr Gln Gly Glu Asp Thr Leu Leu Val Met
1235 1240 1245

Phe Tyr Asn Gln Gln Asp Thr Leu Asp Ser Tyr Lys Asn Ala Ser Met
1250 1255 1260

25 Gln Gly Leu Tyr Ile Phe Ala Asp Met Ala Ser Lys Asp Met Thr Pro
1265 1270 1275 1280

Glu Gln Ser Asn Val Tyr Arg Asp Asn Ser Tyr Gln Gln Phe Asp Thr
1285 1290 1295

30 Asn Asn Val Arg Arg Val Asn Asn Arg Tyr Ala Glu Asp Tyr Glu Ile
1300 1305 1310

35 Pro Ser Ser Val Ser Ser Arg Lys Asp Tyr Gly Trp Gly Asp Tyr Tyr
1315 1320 1325

Leu Ser Met Val Tyr Asn Gly Asp Ile Pro Thr Ile Asn Tyr Lys Ala
1330 1335 1340

40 Ala Ser Ser Asp Leu Lys Ile Tyr Ile Ser Pro Lys Leu Arg Ile Ile
1345 1350 1355 1360

His Asn Gly Tyr Glu Gly Gln Lys Arg Asn Gln Cys Asn Leu Met Asn
1365 1370 1375

45 Lys Tyr Gly Lys Leu Gly Asp Lys Phe Ile Val Tyr Thr Ser Leu Gly
1380 1385 1390

50 Val Asn Pro Asn Asn Ser Ser Asn Lys Leu Met Phe Tyr Pro Val Tyr
1395 1400 1405

Gln Tyr Ser Gly Asn Thr Ser Gly Leu Asn Gln Gly Arg Leu Leu Phe
1410 1415 1420

55 His Arg Asp Thr Thr Tyr Pro Ser Lys Val Glu Ala Trp Ile Pro Gly
1425 1430 1435 1440

Ala Lys Arg Ser Leu Thr Asn Gln Asn Ala Ala Ile Gly Asp Asp Tyr
1445 1450 1455

60 Ala Thr Asp Ser Leu Asn Lys Pro Asp Asp Leu Lys Gln Tyr Ile Phe
1460 1465 1470

65 Met Thr Asp Ser Lys Gly Thr Ala Thr Asp Val Ser Gly Pro Val Glu
1475 1480 1485

Ile Asn Thr Ala Ile Ser Pro Ala Lys Val Gln Ile Ile Val Lys Ala
1490 1495 1500

70 Gly Gly Lys Glu Gln Thr Phe Thr Ala Asp Lys Asp Val Ser Ile Gln

	1505	1510	1515	1520
	Pro Ser Pro Ser Phe Asp Glu Met Asn Tyr Gln Phe Asn Ala Leu Glu			
5	1525		1530	1535
	Ile Asp Gly Ser Gly Leu Asn Phe Ile Asn Asn Ser Ala Ser Ile Asp			
	1540	1545		1550
10	Val Thr Phe Thr Ala Phe Ala Glu Asp Gly Arg Lys Leu Gly Tyr Glu			
	1555	1560		1565
	Ser Phe Ser Ile Pro Val Thr Leu Lys Val Ser Thr Asp Asn Ala Leu			
	1570	1575	1580	
15	Thr Leu His His Asn Glu Asn Gly Ala Gln Tyr Met Gln Trp Gln Ser			
	1585	1590	1595	1600
	Tyr Arg Thr Arg Leu Asn Thr Leu Phe Ala Arg Gln Leu Val Ala Arg			
20		1605	1610	1615
	Ala Thr Thr Gly Ile Asp Thr Ile Leu Ser Met Glu Thr Gln Asn Ile			
	1620	1625		1630
25	Gln Glu Pro Gln Leu Gly Lys Gly Phe Tyr Ala Thr Phe Val Ile Pro			
	1635	1640		1645
	Pro Tyr Asn Leu Ser Thr His Gly Asp Glu Arg Trp Phe Lys Leu Tyr			
	1650	1655	1660	
30	Ile Lys His Val Val Asp Asn Asn Ser His Ile Ile Tyr Ser Gly Gln			
	1665	1670	1675	1680
	Leu Thr Asp Thr Asn Ile Asn Ile Thr Leu Phe Ile Pro Leu Asp Asp			
35		1685	1690	1695
	Val Pro Leu Asn Gln Asp Tyr His Ala Lys Val Tyr Met Thr Phe Lys			
	1700	1705		1710
40	Lys Ser Pro Ser Asp Gly Thr Trp Trp Gly Pro His Phe Val Arg Asp			
	1715	1720		1725
	Asp Lys Gly Ile Val Thr Ile Asn Pro Lys Ser Ile Leu Thr His Phe			
	1730	1735	1740	
45	Glu Ser Val Asn Val Leu Asn Asn Ile Ser Ser Glu Pro Met Asp Phe			
	1745	1750	1755	1760
	Ser Gly Ala Asn Ser Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro			
50		1765	1770	1775
	Met Leu Val Ala Gln Arg Leu Leu His Glu Gln Asn Phe Asp Glu Ala			
	1780	1785		1790
55	Asn Arg Trp Leu Lys Tyr Val Trp Ser Pro Ser Gly Tyr Ile Val His			
	1795	1800	1805	
	Gly Gln Ile Gln Asn Tyr Gln Trp Asn Val Arg Pro Leu Leu Glu Asp			
	1810	1815	1820	
60	Thr Ser Trp Asn Ser Asp Pro Leu Asp Ser Val Asp Pro Asp Ala Val			
	1825	1830	1835	1840
	Ala Gln His Asp Pro Met His Tyr Lys Val Ser Thr Phe Met Arg Thr			
65		1845	1850	1855
	Leu Asp Leu Leu Ile Ala Arg Gly Asp His Ala Tyr Arg Gln Leu Glu			
	1860	1865		1870
70	Arg Asp Thr Leu Asn Glu Ala Lys Met Trp Tyr Met Gln Ala Leu His			
	1875	1880	1885	

	Leu	Leu	Gly	Asp	Lys	Pro	Tyr	Leu	Pro	Leu	Ser	Thr	Thr	Trp	Ser	Asp	
	1390						1895					1900					
5	Pro	Arg	Leu	Asp	Arg	Ala	Ala	Asp	Ile	Thr	Thr	Gln	Asn	Ala	His	Asp	
	1905					1910				1915					1920		
	Ser	Ala	Ile	Val	Ala	Leu	Arg	Gln	Asn	Ile	Pro	Thr	Pro	Ala	Pro	Leu	
					1925					1930					1935		
10	Ser	Leu	Arg	Ser	Ala	Asn	Thr	Leu	Thr	Asp	Leu	Phe	Leu	Pro	Gln	Ile	
				1940					1945					1950			
	Asn	Glu	Val	Met	Met	Asn	Tyr	Trp	Gln	Thr	Leu	Ala	Gln	Arg	Val	Tyr	
			1955					1960						1965			
15	Asn	Leu	Arg	His	Asn	Leu	Ser	Ile	Asp	Gly	Gln	Pro	Leu	Tyr	Leu	Pro	
		1970					1975					1980					
	Ile	Tyr	Ala	Thr	Pro	Ala	Asp	Pro	Lys	Ala	Leu	Leu	Ser	Ala	Ala	Val	
20		1985				1990					1995					2000	
	Ala	Thr	Ser	Gln	Gly	Gly	Gly	Lys	Leu	Pro	Glu	Ser	Phe	Met	Ser	Leu	
					2005					2010					2015		
25	Trp	Arg	Phe	Pro	His	Met	Leu	Glu	Asn	Ala	Arg	Gly	Met	Val	Ser	Gln	
				2020					2025					2030			
	Leu	Thr	Gln	Phe	Gly	Ser	Thr	Leu	Gln	Asn	Ile	Ile	Glu	Arg	Gln	Asp	
			2035					2040					2045				
30	Ala	Glu	Ala	Leu	Asn	Ala	Leu	Leu	Gln	Asn	Gln	Ala	Ala	Glu	Leu	Ile	
		2050					2055					2060					
	Leu	Thr	Asn	Leu	Ser	Ile	Gln	Asp	Lys	Thr	Ile	Glu	Glu	Leu	Asp	Ala	
35		2065				2070				2075						2080	
	Glu	Lys	Thr	Val	Leu	Glu	Lys	Ser	Lys	Ala	Gly	Ala	Gln	Ser	Arg	Phe	
				2085					2090						2095		
40	Asp	Ser	Tyr	Gly	Lys	Leu	Tyr	Asp	Glu	Asn	Ile	Asn	Ala	Gly	Glu	Asn	
			2100					2105						2110			
	Gln	Ala	Met	Thr	Leu	Arg	Ala	Ser	Ala	Ala	Gly	Leu	Thr	Thr	Ala	Val	
			2115					2120					2125				
45	Gln	Ala	Ser	Arg	Leu	Ala	Gly	Ala	Ala	Ala	Asp	Leu	Val	Pro	Asn	Ile	
		2130					2135					2140					
	Phe	Gly	Phe	Ala	Gly	Gly	Gly	Ser	Arg	Trp	Gly	Ala	Ile	Ala	Glu	Ala	
50		2145				2150				2155						2160	
	Thr	Gly	Tyr	Val	Met	Glu	Phe	Ser	Ala	Asn	Val	Met	Asn	Thr	Glu	Ala	
				2165					2170						2175		
55	Asp	Lys	Ile	Ser	Gln	Ser	Glu	Thr	Tyr	Arg	Arg	Arg	Arg	Gln	Glu	Trp	
			2180						2185					2190			
	Glu	Ile	Gln	Arg	Asn	Asn	Ala	Glu	Ala	Glu	Leu	Lys	Gln	Ile	Asp	Ala	
		2195					2200						2205				
60	Gln	Leu	Lys	Ser	Leu	Ala	Val	Arg	Arg	Glu	Ala	Ala	Val	Leu	Gln	Lys	
		2210					2215						2220				
	Thr	Ser	Leu	Lys	Thr	Gln	Gln	Glu	Gln	Thr	Gln	Ser	Gln	Leu	Ala	Phe	
65		2225				2230				2235						2240	
	Leu	Gln	Arg	Lys	Phe	Ser	Asn	Gln	Ala	Leu	Tyr	Asn	Trp	Leu	Arg	Gly	
				2245					2250						2255		
70	Arg	Leu	Ala	Ala	Ile	Tyr	Phe	Gln	Phe	Tyr	Asp	Leu	Ala	Val	Ala	Arg	
			2260						2265					2270			

Cys Leu Met Ala Glu Gln Ala Tyr Arg Trp Glu Leu Asn Asp Asp Ser
 2275 2280 2285
 5 Ala Arg Phe Ile Lys Pro Gly Ala Trp Gln Gly Thr Tyr Ala Gly Leu
 2290 2295 2300
 Leu Ala Gly Glu Thr Leu Met Leu Ser Leu Ala Gln Met Glu Asp Ala
 2305 2310 2315 2320
 10 His Leu Lys Arg Asp Lys Arg Ala Leu Glu Val Glu Arg Thr Val Ser
 2325 2330 2335
 Leu Ala Glu Val Tyr Ala Gly Leu Pro Lys Asp Asn Gly Pro Phe Ser
 2340 2345 2350
 Leu Ala Gln Glu Ile Asp Lys Leu Val Ser Gln Gly Ser Gly Ser Ala
 2355 2360 2365
 20 Gly Ser Gly Asn Asn Asn Leu Ala Phe Gly Ala Gly Thr Asp Thr Lys
 2370 2375 2380
 Thr Ser Leu Gln Ala Ser Val Ser Phe Ala Asp Leu Lys Ile Arg Glu
 2385 2390 2395 2400
 25 Asp Tyr Pro Ala Ser Leu Gly Lys Ile Arg Arg Ile Lys Gln Ile Ser
 2405 2410 2415
 Val Thr Leu Pro Ala Leu Leu Gly Pro Tyr Gln Asp Val Gln Ala Ile
 2420 2425 2430
 Leu Ser Tyr Gly Asp Lys Ala Gly Leu Ala Asn Gly Cys Glu Ala Leu
 2435 2440 2445
 35 Ala Val Ser His Gly Met Asn Asp Ser Gly Gln Phe Gln Leu Asp Phe
 2450 2455 2460
 Asn Asp Gly Lys Phe Leu Pro Phe Glu Gly Ile Ala Ile Asp Gln Gly
 2465 2470 2475 2480
 40 Thr Leu Thr Leu Ser Phe Pro Asn Ala Ser Met Pro Glu Lys Gly Lys
 2485 2490 2495
 Gln Ala Thr Met Leu Lys Thr Leu Asn Asp Ile Ile Leu His Ile Arg
 2500 2505 2510
 45 Tyr Thr Ile Lys
 2516

50

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5547 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48 (tcdAii coding region):

65 CTG ATA GGC TAT AAC AAT CAA TTT AGC GGT AGA GCC AGT CAA TAT GTT 48
 Leu Ile Gly Tyr Asn Asn Gln Phe Ser Gly Arg Ala Ser Gln Tyr Val
 1 5 10 15
 GCG CCG GGT ACC GTT TCT TCC ATG TTC TCC CCC GCC GCT TAT TTG ACT 96
 Ala Pro Gly Thr Val Ser Ser Met Phe Ser Pro Ala Ala Tyr Leu Thr
 20 25 30

5 GAA CTT TAT CGT GAA GCA CGC AAT TTA CAC GCA AGT GAC TCC GTT TAT 144
 Glu Leu Tyr Arg Glu Ala Arg Asn Leu His Ala Ser Asp Ser Val Tyr
 35 40 45
 TAT CTG GAT ACC CGC CGC CCA GAT CTC AAA TCA ATG GCG CTC AGT CAG 192
 Tyr Leu Asp Thr Arg Arg Pro Asp Leu Lys Ser Met Ala Leu Ser Gln
 50 55 60
 10 CAA AAT ATG GAT ATA GAA TTA TCC ACA CTC TCT TTG TCC AAT GAG CTG 240
 Gln Asn Met Asp Ile Glu Leu Ser Thr Leu Ser Leu Ser Asn Glu Leu
 65 70 75 80
 15 TTA TTG GAA AGC ATT AAA ACT GAA TCT AAA CTG GAA AAC TAT ACT AAA 288
 Leu Leu Glu Ser Ile Lys Thr Glu Ser Lys Leu Glu Asn Tyr Thr Lys
 85 90 95
 20 GTG ATG GAA ATG CTC TCC ACT TTC CGT CCT TCC GGC GCA ACG CCT TAT 336
 Val Met Glu Met Leu Ser Thr Phe Arg Pro Ser Gly Ala Thr Pro Tyr
 100 105 110
 25 CAT GAT GCT TAT GAA AAT GTG CGT GAA GTT ATC CAG CTA CAA GAT CCT 384
 His Asp Ala Tyr Glu Asn Val Arg Glu Val Ile Gln Leu Gln Asp Pro
 115 120 125
 GGA CTT GAG CAA CTC AAT GCA TCA CCG GCA ATT GCC GGG TTG ATG CAT 432
 Gly Leu Glu Gln Leu Asn Ala Ser Pro Ala Ile Ala Gly Leu Met His
 130 135 140
 30 CAA GCC TCC CTA TTG GGT ATT AAC GCT TCA ATC TCG CCT GAG CTA TTT 480
 Gln Ala Ser Leu Leu Gly Ile Asn Ala Ser Ile Ser Pro Glu Leu Phe
 145 150 155 160
 35 AAT ATT CTG ACG GAG GAG ATT ACC GAA GGT AAT GCT GAG GAA CTT TAT 528
 Asn Ile Leu Thr Glu Glu Ile Thr Glu Gly Asn Ala Glu Glu Leu Tyr
 165 170 175
 40 AAG AAA AAT TTT GGT AAT ATC GAA CCG GCC TCA TTG GCT ATG CCG GAA 576
 Lys Lys Asn Phe Gly Asn Ile Glu Pro Ala Ser Leu Ala Met Pro Glu
 180 185 190
 45 TAC CTT AAA CGT TAT TAT AAT TTA AGC GAT GAA GAA CTT AGT CAG TTT 624
 Tyr Leu Lys Arg Tyr Tyr Asn Leu Ser Asp Glu Glu Leu Ser Gln Phe
 195 200 205
 ATT GGT AAA GCC AGC AAT TTT GGT CAA CAG GAA TAT AGT AAT AAC CAA 672
 Ile Gly Lys Ala Ser Asn Phe Gly Gln Gln Glu Tyr Ser Asn Asn Gln
 210 215 220
 50 CTT ATT ACT CCG GTA GTC AAC AGC AGT GAT GGC ACG GTT AAG GTA TAT 720
 Leu Ile Thr Pro Val Val Asn Ser Ser Asp Gly Thr Val Lys Val Tyr
 225 230 235 240
 55 CGG ATC ACC CGC GAA TAT ACA ACC AAT GCT TAT CAA ATG GAT GTG GAG 768
 Arg Ile Thr Arg Glu Tyr Thr Thr Asn Ala Tyr Gln Met Asp Val Glu
 245 250 255
 60 CTA TTT CCC TTC GGT GGT GAG AAT TAT CGG TTA GAT TAT AAA TTC AAA 816
 Leu Phe Pro Phe Gly Gly Glu Asn Tyr Arg Leu Asp Tyr Lys Phe Lys
 260 265 270
 65 AAT TTT TAT AAT GCC TCT TAT TTA TCC ATC AAG TTA AAT GAT AAA AGA 864
 Asn Phe Tyr Asn Ala Ser Tyr Leu Ser Ile Lys Leu Asn Asp Lys Arg
 275 280 285
 GAA CTT GTT CGA ACT GAA GGC GCT CCT CAA GTC AAT ATA GAA TAC TCC 912
 Glu Leu Val Arg Thr Glu Gly Ala Pro Gln Val Asn Ile Glu Tyr Ser
 290 295 300
 70 GCA AAT ATC ACA TTA AAT ACC GCT GAT ATC AGT CAA CCT TTT GAA ATT 960
 Ala Asn Ile Thr Leu Asn Thr Ala Asp Ile Ser Gln Pro Phe Glu Ile

305 310 315 320
 5 GGC CTG ACA CGA GTA CTT CCT TCC GGT TCT TGG GCA TAT GCC GCC GCA 1008
 Gly Leu Thr Arg Val Leu Pro Ser Gly Ser Trp Ala Tyr Ala Ala Ala
 325 330 335
 10 AAA TTT ACC GTT GAA GAG TAT AAC CAA TAC TCT TTT CTG CTA AAA CTT 1056
 Lys Phe Thr Val Glu Glu Tyr Asn Gln Tyr Ser Phe Leu Leu Lys Leu
 340 345 350
 AAC AAG GCT ATT CCT CTA TCA CGT GCG ACA GAA TTG TCA CCC ACG ATT 1104
 Asn Lys Ala Ile Arg Leu Ser Arg Ala Thr Glu Leu Ser Pro Thr Ile
 355 360 365
 15 CTG GAA GGC ATT GTG CGC AGT GTT AAT CTA CAA CTG GAT ATC AAC ACA 1152
 Leu Glu Gly Ile Val Arg Ser Val Asn Leu Gln Leu Asp Ile Asn Thr
 370 375 380
 20 GAC GTA TTA GGT AAA GTT TTT CTG ACT AAA TAT TAT ATG CAG CGT TAT 1200
 Asp Val Leu Gly Lys Val Phe Leu Thr Lys Tyr Tyr Met Gln Arg Tyr
 385 390 395 400
 25 GCT ATT CAT GCT GAA ACT GCC CTG ATA CTA TGC AAC GCG CCT ATT TCA 1248
 Ala Ile His Ala Glu Thr Ala Leu Ile Leu Cys Asn Ala Pro Ile Ser
 405 410 415
 CAA CGT TCA TAT GAT AAT CAA CCT AGC CAA TTT GAT CGC CTG TTT AAT 1296
 Gln Arg Ser Tyr Asp Asn Gln Pro Ser Gln Phe Asp Arg Leu Phe Asn
 420 425 430
 30 ACG CCA TTA CTG AAC GGA CAA TAT TTT TCT ACC GGC GAT GAG GAG ATT 1344
 Thr Pro Leu Leu Asn Gly Gln Tyr Phe Ser Thr Gly Asp Glu Glu Ile
 435 440 445
 35 GAT TTA AAT TCA GGT AGC ACC GGC GAT TGG CGA AAA ACC ATA CTT AAG 1392
 Asp Leu Asn Ser Gly Ser Thr Gly Asp Trp Arg Lys Thr Ile Leu Lys
 450 455 460
 40 CGT GCA TTT AAT ATT GAT GAT GTC TCG CTC TTC CGC CTG CTT AAA ATT 1440
 Arg Ala Phe Asn Ile Asp Asp Val Ser Leu Phe Arg Leu Leu Lys Ile
 465 470 475 480
 45 ACC GAC CAT GAT AAT AAA GAT GGA AAA ATT AAA AAT AAC CTA AAG AAT 1488
 Thr Asp His Asp Asn Lys Asp Gly Lys Ile Lys Asn Asn Leu Lys Asn
 485 490 495
 50 CTT TCC AAT TTA TAT ATT GGA AAA TTA CTG GCA GAT ATT CAT CAA TTA 1536
 Leu Ser Asn Leu Tyr Ile Gly Lys Leu Leu Ala Asp Ile His Gln Leu
 500 505 510
 ACC ATT GAT GAA CTG GAT TTA TTA CTG ATT GCC GTA GGT GAA GGA AAA 1584
 Thr Ile Asp Glu Leu Asp Leu Leu Ile Ala Val Gly Glu Gly Lys
 515 520 525
 55 ACT AAT TTA TCC GCT ATC AGT GAT AAG CAA TTG GCT ACC CTG ATC AGA 1632
 Thr Asn Leu Ser Ala Ile Ser Asp Lys Gln Leu Ala Thr Leu Ile Arg
 530 535 540
 60 AAA CTC AAT ACT ATT ACC AGC TGG CTA CAT ACA CAG AAG TGG AGT GTA 1680
 Lys Leu Asn Thr Ile Thr Ser Trp Leu His Thr Gln Lys Trp Ser Val
 545 550 555 560
 65 TTC CAG CTA TTT ATC ATG ACC TCC ACC AGC TAT AAC AAA ACG CTA ACG 1728
 Phe Gln Leu Phe Ile Met Thr Ser Thr Ser Tyr Asn Lys Thr Leu Thr
 565 570 575
 70 CCT GAA ATT AAG AAT TTG CTG GAT ACC GTC TAC CAC GGT TTA CAA GGT 1776
 Pro Glu Ile Lys Asn Leu Leu Asp Thr Val Tyr His Gly Leu Gln Gly
 580 585 590
 TTT GAT AAA GAC AAA GCA GAT TTG CTA CAT GTC ATG GCG CCC TAT ATT 1824

	Phe	Asp	Lys	Asp	Lys	Ala	Asp	Leu	Leu	His	Val	Met	Ala	Pro	Tyr	Ile	
			595					600					605				
5	GCG	GCC	ACC	TTG	CAA	TTA	TCA	TCG	GAA	AAT	GTC	GCC	CAC	TCG	GTA	CTC	1372
	Ala	Ala	Thr	Leu	Gln	Leu	Ser	Ser	Glu	Asn	Val	Ala	His	Ser	Val	Leu	
			610				615					620					
10	CTT	TGG	GCA	GAT	AAG	TTA	CAG	CCC	GGC	GAC	GGC	GCA	ATG	ACA	GCA	GAA	1920
	Leu	Trp	Ala	Asp	Lys	Leu	Gln	Pro	Gly	Asp	Gly	Ala	Met	Thr	Ala	Glu	
						630					635					640	
15	AAA	TTC	TGG	GAC	TGG	TTG	AAT	ACT	AAG	TAT	ACG	CCG	GGT	TCA	TCG	GAA	1963
	Lys	Phe	Trp	Asp	Trp	Leu	Asn	Thr	Lys	Tyr	Thr	Pro	Gly	Ser	Ser	Glu	
					645				650						655		
20	GCC	GTA	GAA	ACG	CAG	GAA	CAT	ATC	GTT	CAG	TAT	TGT	CAG	GCT	CTG	GCA	2016
	Ala	Val	Glu	Thr	Gln	Glu	His	Ile	Val	Gln	Tyr	Cys	Gln	Ala	Leu	Ala	
				660				665						670			
25	CAA	TTG	GAA	ATG	GTT	TAC	CAT	TCC	ACC	GGC	ATC	AAC	GAA	AAC	GCC	TTC	2064
	Gln	Leu	Glu	Met	Val	Tyr	His	Ser	Thr	Gly	Ile	Asn	Glu	Asn	Ala	Phe	
			675					680					685				
30	CGT	CTA	TTT	GTG	ACA	AAA	CCA	GAG	ATG	TTT	GGC	GCT	GCA	ACT	GGA	GCA	2112
	Arg	Leu	Phe	Val	Thr	Lys	Pro	Glu	Met	Phe	Gly	Ala	Ala	Thr	Gly	Ala	
			690				695					700					
35	GCG	CCC	GCG	CAT	GAT	GCC	CTT	TCA	CTG	ATT	ATG	CTG	ACA	CGT	TTT	GCG	2160
	Ala	Pro	Ala	His	Asp	Ala	Leu	Ser	Leu	Ile	Met	Leu	Thr	Arg	Phe	Ala	
			705			710				715					720		
40	GAT	TGG	GTG	AAC	GCA	CTA	GGC	GAA	AAA	GCG	TCC	TCG	GTG	CTA	GCG	GCA	2208
	Asp	Trp	Val	Asn	Ala	Leu	Gly	Glu	Lys	Ala	Ser	Ser	Val	Leu	Ala	Ala	
				725				730						735			
45	TTT	GAA	GCT	AAC	TCG	TTA	ACG	GCA	GAA	CAA	CTG	GCT	GAT	GCC	ATG	AAT	2256
	Phe	Glu	Ala	Asn	Ser	Leu	Thr	Ala	Glu	Gln	Leu	Ala	Asp	Ala	Met	Asn	
				740				745					750				
50	CTT	GAT	GCT	AAT	TTG	CTG	TTG	CAA	GCC	AGT	ATT	CAA	GCA	CAA	AAT	CAT	2304
	Leu	Asp	Ala	Asn	Leu	Leu	Leu	Gln	Ala	Ser	Ile	Gln	Ala	Gln	Asn	His	
			755				760					765					
55	CAA	CAT	CTT	CCC	CCA	GTA	ACT	CCA	GAA	AAT	GCG	TTC	TCC	TGT	TGG	ACA	2352
	Gln	His	Leu	Pro	Pro	Val	Thr	Pro	Glu	Asn	Ala	Phe	Ser	Cys	Trp	Thr	
			770				775					780					
60	TCT	ATC	AAT	ACT	ATC	CTG	CAA	TGG	GTT	AAT	GTC	GCA	CAA	CAA	TTG	AAT	2400
	Ser	Ile	Asn	Thr	Ile	Leu	Gln	Trp	Val	Asn	Val	Ala	Gln	Gln	Leu	Asn	
			785			790					795				800		
65	GTC	GCC	CCA	CAG	GGC	GTT	TCC	GCT	TTG	GTC	GGG	CTG	GAT	TAT	ATT	CAA	2448
	Val	Ala	Pro	Gln	Gly	Val	Ser	Ala	Leu	Val	Gly	Leu	Asp	Tyr	Ile	Gln	
				805						810					815		
70	TCA	ATG	AAA	GAG	ACA	CCG	ACC	TAT	GCC	CAG	TGG	GAA	AAC	GCG	GCA	GGC	2496
	Ser	Met	Lys	Glu	Thr	Pro	Thr	Tyr	Ala	Gln	Trp	Glu	Asn	Ala	Ala	Gly	
				820				825						830			
75	GTA	TTA	ACC	GCC	GGG	TTG	AAT	TCA	CAA	CAG	GCT	AAT	ACA	TTA	CAC	GCT	2544
	Val	Leu	Thr	Ala	Gly	Leu	Asn	Ser	Gln	Gln	Ala	Asn	Thr	Leu	His	Ala	
			835				840						845				
80	TTT	CTG	GAT	GAA	TCT	CGC	AGT	GCC	GCA	TTA	AGC	ACC	TAC	TAT	ATC	CGT	2592
	Phe	Leu	Asp	Glu	Ser	Arg	Ser	Ala	Ala	Leu	Ser	Thr	Tyr	Tyr	Ile	Arg	
			850			855						860					
85	CAA	GTC	GCC	AAG	GCA	GCG	GCG	GCT	ATT	AAA	AGC	CGT	GAT	GAC	TTG	TAT	2640
	Gln	Val	Ala	Lys	Ala	Ala	Ala	Ala	Ile	Lys	Ser	Arg	Asp	Asp	Leu	Tyr	
			865			870					875				880		

CAA TAC TTA CTG ATT GAT AAT CAG GTT TCT GCG GCA ATA AAA ACC ACC 2888
 Gln Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Ala Ile Lys Thr Thr
 385 890 895

5 CGG ATC GCC GAA GCC ATT GCC AGT ATT CAA CTG TAC CTC AAC CGG GCA 2736
 Arg Ile Ala Glu Ala Ile Ala Ser Ile Gln Leu Tyr Val Asn Arg Ala
 900 905 910

10 TTG GAA AAT GTG GAA GAA AAT GCC AAT TCG GGG GTT ATC AGC CGC CAA 2784
 Leu Glu Asn Val Glu Glu Asn Ala Asn Ser Gly Val Ile Ser Arg Gln
 915 920 925

15 TTC TTT ATC GAC TGG GAC AAA TAC AAT AAA CCG TAC AGC ACT TGG GCG 2832
 Phe Phe Ile Asp Trp Asp Lys Tyr Asn Lys Arg Tyr Ser Thr Trp Ala
 930 935 940

20 GGT GTT TCT CAA TTA GTT TAC TAC CCG GAA AAC TAT ATT GAT CCG ACC 2980
 Gly Val Ser Gln Leu Val Tyr Tyr Pro Glu Asn Tyr Ile Asp Pro Thr
 945 950 955 960

25 ATG CGT ATC GGA CAA ACC AAA ATG ATG GAC GCA TTA CTG CAA TCC GTC 2928
 Met Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu Gln Ser Val
 965 970 975

30 AGC CAA AGC CAA TTA AAC GCC GAT ACC GTC GAA GAT GCC TTT ATG TCT 2976
 Ser Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala Phe Met Ser
 980 985 990

35 TAT CTG ACA TCG TTT GAA CAA CTG GCT AAT CTT AAA GTT ATT AGC GCA 3024
 Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val Ile Ser Ala
 995 1000 1005

40 TAT CAC GAT AAT ATT AAT AAC GAT CAA GGG CTG ACC TAT TTT ATC GGA 3072
 Tyr His Asp Asn Ile Asn Asn Asp Gln Gly Leu Thr Tyr Phe Ile Gly
 1010 1015 1020

45 CTC AGT GAA ACT GAT GCC GGT GAA TAT TAT TGG CCG AGT GTC GAT CAC 3120
 Leu Ser Glu Thr Asp Ala Gly Glu Tyr Tyr Trp Arg Ser Val Asp His
 1025 1030 1035 1040

50 AGT AAA TTC AAC GAC GGT AAA TTC GCG GCT AAT GCC TGG AGT GAA TGG 3168
 Ser Lys Phe Asn Asp Gly Lys Phe Ala Ala Asn Ala Trp Ser Glu Trp
 1045 1050 1055

55 CAT AAA ATT GAT TGT CCA ATT AAC CCT TAT AAA AGC ACT ATC CGT CCA 3216
 His Lys Ile Asp Cys Pro Ile Asn Pro Tyr Lys Ser Thr Ile Arg Pro
 1060 1065 1070

60 GTG ATA TAT AAA TCC CGC CTG TAT CTG CTC TGG TTG GAA CAA AAG GAG 3264
 Val Ile Tyr Lys Ser Arg Leu Tyr Leu Leu Trp Leu Glu Gln Lys Glu
 1075 1080 1085

65 ATC ACC AAA CAG ACA GGA AAT AGT AAA GAT GGC TAT CAA ACT GAA ACG 3312
 Ile Thr Lys Gln Thr Gly Asn Ser Lys Asp Gly Tyr Gln Thr Glu Thr
 1090 1095 1100

70 GAT TAT CGT TAT GAA CTA AAA TTG GCG CAT ATC CGC TAT GAT GGC ACT 3360
 Asp Tyr Arg Tyr Glu Leu Lys Leu Ala His Ile Arg Tyr Asp Gly Thr
 1105 1110 1115 1120

TGG AAT ACG CCA ATC ACC TTT GAT GTC AAT AAA AAA ATA TCC GAG CTA 3408
 Trp Asn Thr Pro Ile Thr Phe Asp Val Asn Lys Lys Ile Ser Glu Leu
 1125 1130 1135

75 AAA CTG GAA AAA AAT AGA GCG CCC GGA CTC TAT TGT GCC GGT TAT CAA 3456
 Lys Leu Glu Lys Asn Arg Ala Pro Gly Leu Tyr Cys Ala Gly Tyr Gln
 1140 1145 1150

80 GGT GAA GAT ACG TTG CTG GTG ATG TTT TAT AAC CAA CAA GAC ACA CTA 3504
 Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Asn Gln Gln Asp Thr Leu
 1155 1160 1165

5 GAT AGT TAT AAA AAC GCT TCA ATG CAA GGA CTA TAT ATC TTT GCT GAT 3552
 Asp Ser Tyr Lys Asn Ala Ser Met Gln Gly Leu Tyr Ile Phe Ala Asp
 1170 1175 1180

10 ATG GCA TCC AAA GAT ATG ACC CCA GAA CAG AGC AAT GTT TAT CGG GAT 3600
 Met Ala Ser Lys Asp Met Thr Pro Glu Gln Ser Asn Val Tyr Arg Asp
 1185 1190 1195 1200

15 AAT AGC TAT CAA CAA TTT GAT ACC AAT AAT GTC AGA AGA CTG AAT AAC 3648
 Asn Ser Tyr Gln Gln Phe Asp Thr Asn Asn Val Arg Arg Val Asn Asn
 1205 1210 1215

20 CGC TAT GCA GAG GAT TAT GAG ATT CCT TCC TCG GTA AGT AGC CGT AAA 3696
 Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Ser Ser Arg Lys
 1220 1225 1230

25 GAC TAT GGT TGG GGA GAT TAT TAC CTC AGC ATG GTA TAT AAC GGA GAT 3744
 Asp Tyr Gly Trp Gly Asp Tyr Tyr Leu Ser Met Val Tyr Asn Gly Asp
 1235 1240 1245

30 ATT CCA ACT ATC AAT TAC AAA GCC GCA TCA AGT GAT TTA AAA ATC TAT 3792
 Ile Pro Thr Ile Asn Tyr Lys Ala Ala Ser Ser Asp Leu Lys Ile Tyr
 1250 1255 1260

35 ATC TCA CCA AAA TTA AGA ATT ATT CAT AAT GGA TAT GAA GGA CAG AAG 3840
 Ile Ser Pro Lys Leu Arg Ile Ile His Asn Gly Tyr Glu Gly Gln Lys
 1265 1270 1275 1280

40 CGC AAT CAA TGC AAT CTG ATG AAT AAA TAT GGC AAA CTA GGT GAT AAA 3888
 Arg Asn Gln Cys Asn Leu Met Asn Lys Tyr Gly Lys Leu Gly Asp Lys
 1285 1290 1295

45 TTT ATT GTT TAT ACT AGC TTG GGG GTC AAT CCA AAT AAC TCG TCA AAT 3936
 Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn Ser Ser Asn
 1300 1305 1310

50 AAG CTC ATG TTT TAC CCC GTC TAT CAA TAT AGC GGA AAC ACC AGT GGA 3984
 Lys Leu Met Phe Tyr Pro Val Tyr Gln Tyr Ser Gly Asn Thr Ser Gly
 1315 1320 1325

55 CTC AAT CAA GGG AGA CTA CTA TTC CAC CGT GAC ACC ACT TAT CCA TCT 4032
 Leu Asn Gln Gly Arg Leu Leu Phe His Arg Asp Thr Thr Tyr Pro Ser
 1330 1335 1340

60 AAA GTA GAA GCT TGG ATT CCT GGA GCA AAA CGT TCT CTA ACC AAC CAA 4080
 Lys Val Glu Ala Trp Ile Pro Gly Ala Lys Arg Ser Leu Thr Asn Gln
 1345 1350 1355 1360

65 AAT GCC GCC ATT GGT GAT GAT TAT GCT ACA GAC TCT CTG AAT AAA CCG 4128
 Asn Ala Ala Ile Gly Asp Asp Tyr Ala Thr Asp Ser Leu Asn Lys Pro
 1365 1370 1375

70 GAT GAT CTT AAG CAA TAT ATC TTT ATG ACT GAC AGT AAA GGG ACT GCT 4176
 Asp Asp Leu Lys Gln Tyr Ile Phe Met Thr Asp Ser Lys Gly Thr Ala
 1380 1385 1390

75 ACT GAT GTC TCA GGC CCA GTA GAG ATT AAT ACT GCA ATT TCT CCA GCA 4224
 Thr Asp Val Ser Gly Pro Val Glu Ile Asn Thr Ala Ile Ser Pro Ala
 1395 1400 1405

80 AAA GTT CAG ATA ATA GTC AAA GCG GGT GGC AAG GAG CAA ACT TTT ACC 4272
 Lys Val Gln Ile Ile Val Lys Ala Gly Gly Lys Glu Gln Thr Phe Thr
 1410 1415 1420

85 GCA GAT AAA GAT GTC TCC ATT CAG CCA TCA CCT AGC TTT GAT GAA ATG 4320
 Ala Asp Lys Asp Val Ser Ile Gln Pro Ser Pro Ser Phe Asp Glu Met
 1425 1430 1435 1440

90 AAT TAT CAA TTT AAT GCC CTT GAA ATA GAC GGT TCT GGT CTG AAT TTT 4368
 Asn Tyr Gln Phe Asn Ala Leu Glu Ile Asp Gly Ser Gly Leu Asn Phe

	1445	1450	1455	
5	ATT AAC AAC TCA GCC AGT ATT GAT GTT ACT TTT ACC GCA TTT GCG GAG 4416 Ile Asn Asn Ser Ala Ser Ile Asp Val Thr Phe Thr Ala Phe Ala Glu 1460 1465 1470			
10	GAT GGC CGC AAA CTG GGT TAT GAA AGT TTC AGT ATT CCT GTT ACC CTC 4464 Asp Gly Arg Lys Leu Gly Tyr Glu Ser Phe Ser Ile Pro Val Thr Leu 1475 1480 1485			
15	AAG GTA AGT ACC GAT AAT GCC CTG ACC CTG CAC CAT AAT GAA AAT GGT 4512 Lys Val Ser Thr Asp Asn Ala Leu Thr Leu His His Asn Glu Asn Gly 1490 1495 1500			
20	GCG CAA TAT ATG CAA TGG CAA TCC TAT CGT ACC CGC CTG AAT ACT CTA 4560 Ala Gln Tyr Met Gln Trp Gln Ser Tyr Arg Thr Arg Leu Asn Thr Leu 1505 1510 1515 1520			
25	TTT GCC CGC CAG TTG GTT GCA CGC GCC ACC ACC GGA ATC GAT ACA ATT 4608 Phe Ala Arg Gln Leu Val Ala Arg Ala Thr Thr Gly Ile Asp Thr Ile 1525 1530 1535			
30	CTG AGT ATG GAA ACT CAG AAT ATT CAG GAA CCG CAG TTA GGC AAA GGT 4656 Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu Gly Lys Gly 1540 1545 1550			
35	TTC TAT GCT ACG TTC GTG ATA CCT CCC TAT AAC CTA TCA ACT CAT GGT 4704 Phe Tyr Ala Thr Phe Val Ile Pro Pro Tyr Asn Leu Ser Thr His Gly 1555 1560 1565			
40	GAT GAA CGT TCG TTT AAG CTT TAT ATC AAA CAT GTT GTT GAT AAT AAT 4752 Asp Glu Arg Trp Phe Lys Leu Tyr Ile Lys His Val Val Asp Asn Asn 1570 1575 1580			
45	TCA CAT ATT ATC TAT TCA GGC CAG CTA ACA GAT ACA AAT ATA AAC ATC 4800 Ser His Ile Ile Tyr Ser Gly Gln Leu Thr Asp Thr Asn Ile Asn Ile 1585 1590 1595 1600			
50	ACA TTA TTT ATT CCT CTT GAT GAT GTC CCA TTG AAT CAA GAT TAT CAC 4848 Thr Leu Phe Ile Pro Leu Asp Asp Val Pro Leu Asn Gln Asp Tyr His 1605 1610 1615			
55	GCC AAG GTT TAT ATG ACC TTC AAG AAA TCA CCA TCA GAT GGT ACC TGG 4896 Ala Lys Val Tyr Met Thr Phe Lys Lys Ser Pro Ser Asp Gly Thr Trp 1620 1625 1630			
60	TGG GGC CCT CAC TTT GTT AGA GAT GAT AAA GGA ATA GTA ACA ATA AAC 4944 Trp Gly Pro His Phe Val Arg Asp Asp Lys Gly Ile Val Thr Ile Asn 1635 1640 1645			
65	CCT AAA TCC ATT TTG ACC CAT TTT GAG AGC GTC AAT GTC CTG AAT AAT 4992 Pro Lys Ser Ile Leu Thr His Phe Glu Ser Val Asn Val Leu Asn Asn 1650 1655 1660			
70	ATT AGT AGC GAA CCA ATG GAT TTC AGC GGC GCT AAC AGC CTC TAT TTC 5040 Ile Ser Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ser Leu Tyr Phe 1665 1670 1675 1680			
	TGG GAA CTG TTC TAC TAT ACC CCG ATG CTG GTT GCT CAA CGT TTG CTG 5088 Trp Glu Leu Phe Tyr Tyr Thr Pro Met Leu Val Ala Gln Arg Leu Leu 1685 1690 1695			
	CAT GAA CAG AAC TTC GAT GAA GCC AAC CGT TGG CTG AAA TAT GTC TGG 5136 His Glu Gln Asn Phe Asp Glu Ala Asn Arg Trp Leu Lys Tyr Val Trp 1700 1705 1710			
	AGT CCA TCC GGT TAT ATT GTC CAC GGC CAG ATT CAG AAC TAC CAG TGG 5184 Ser Pro Ser Gly Tyr Ile Val His Gly Gln Ile Gln Asn Tyr Gln Trp 1715 1720 1725			
	AAC GTC CGC CCG TTA CTG GAA GAC ACC AGT TGG AAC AGT GAT CCT TTG 5232			

Asn Val Arg Pro Leu Leu Glu Asp Thr Ser Trp Asn Ser Asp Pro Leu
 1730 1735 1740
 5 GAT TCC GTC GAT CCT GAC GCG GTA GCA CAG CAC GAT CCA ATG CAC TAC 5230
 Asp Ser Val Asp Pro Asp Ala Val Ala Gln His Asp Pro Met His Tyr
 1745 1750 1755 1760
 10 AAA GTT TCA ACT TTT ATG CGT ACC TTG GAT CTA TTG ATA GCA CGC GGC 5323
 Lys Val Ser Thr Phe Met Arg Thr Leu Asp Leu Leu Ile Ala Arg Gly
 1765 1770 1775
 15 GAC CAT GCT TAT CGC CAA CTG GAA CGA GAT ACA CTC AAC GAA GCG AAG 5376
 Asp His Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Asn Glu Ala Lys
 1780 1785 1790
 ATG TGG TAT ATG CAA GCG CTG CAT CTA TTA GGT GAC AAA CCT TAT CTA 5424
 Met Trp Tyr Met Gln Ala Leu His Leu Leu Gly Asp Lys Pro Tyr Leu
 1795 1800 1805
 20 CCG CTG AGT ACG ACA TGG AGT GAT CCA CGA CTA GAC AGA GCC GCG GAT 5472
 Pro Leu Ser Thr Thr Trp Ser Asp Pro Arg Leu Asp Arg Ala Ala Asp
 1810 1815 1820
 25 ATC ACT ACC CAA AAT GCT CAC GAC AGC GCA ATA GTC GCT CTG CGG CAG 5520
 Ile Thr Thr Gln Asn Ala His Asp Ser Ala Ile Val Ala Leu Arg Gln
 1825 1830 1835 1840
 30 AAT ATA CCT ACA CCG GCA CCT TTA TCA 5547
 Asn Ile Pro Thr Pro Ala Pro Leu Ser
 1845 1849

(2) INFORMATION FOR SEQ ID NO:49:
 (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 1849 amino acids
 (B) TYPE: amino acids
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49 (TcdA_{ii}):
 45 Features From To Description
 Peptide 1 1849 TcdA_{ii} peptide
 Fragment 1 12 S2 N-terminus (SEQ ID NO:13)
 Fragment 196 211 (SEQ ID NO:38)
 Fragment 466 475 (SEQ ID NO:17)
 Fragment 993 1004 (SEQ ID NO:23; 12/13)
 50 Fragment 1297 1312 (SEQ ID NO:18)
 Fragment 1390 1409 (SEQ ID NO:39)
 Fragment 1532 1554 (SEQ ID NO:21; 19/23)

55 Leu Ile Gly Tyr Asn Asn Gln Phe Ser Gly Arg Ala Ser Gln Tyr Val
 1 5 10 15
 Ala Pro Gly Thr Val Ser Ser Met Phe Ser Pro Ala Ala Tyr Leu Thr
 20 25 30
 60 Glu Leu Tyr Arg Glu Ala Arg Asn Leu His Ala Ser Asp Ser Val Tyr
 35 40 45
 Tyr Leu Asp Thr Arg Arg Pro Asp Leu Lys Ser Met Ala Leu Ser Gln
 50 55 60
 65 Gln Asn Met Asp Ile Glu Leu Ser Thr Leu Ser Leu Ser Asn Glu Leu
 65 70 75 80
 Leu Leu Glu Ser Ile Lys Thr Glu Ser Lys Leu Glu Asn Tyr Thr Lys

	85	90	95
	Val Met Glu Met Leu Ser Thr Phe Arg Pro Ser Gly Ala Thr Pro Tyr		
	100	105	110
5	His Asp Ala Tyr Glu Asn Val Arg Glu Val Ile Gln Leu Gln Asp Pro		
	115	120	125
10	Gly Leu Glu Gln Leu Asn Ala Ser Pro Ala Ile Ala Gly Leu Met His		
	130	135	140
	Gln Ala Ser Leu Leu Gly Ile Asn Ala Ser Ile Ser Pro Glu Leu Phe		
	145	150	155
15	Asn Ile Leu Thr Glu Glu Ile Thr Glu Gly Asn Ala Glu Glu Leu Tyr		
	165	170	175
	Lys Lys Asn Phe Gly Asn Ile Glu Pro Ala Ser Leu Ala Met Pro Glu		
	180	185	190
20	Tyr Leu Lys Arg Tyr Tyr Asn Leu Ser Asp Glu Glu Leu Ser Gln Phe		
	195	200	205
25	Ile Gly Lys Ala Ser Asn Phe Gly Gln Gln Glu Tyr Ser Asn Asn Gln		
	210	215	220
	Leu Ile Thr Pro Val Val Asn Ser Ser Asp Gly Thr Val Lys Val Tyr		
	225	230	235
30	Arg Ile Thr Arg Glu Tyr Thr Thr Asn Ala Tyr Gln Met Asp Val Glu		
	245	250	255
	Leu Phe Pro Phe Gly Gly Glu Asn Tyr Arg Leu Asp Tyr Lys Phe Lys		
	260	265	270
35	Asn Phe Tyr Asn Ala Ser Tyr Leu Ser Ile Lys Leu Asn Asp Lys Arg		
	275	280	285
40	Glu Leu Val Arg Thr Glu Gly Ala Pro Gln Val Asn Ile Glu Tyr Ser		
	290	295	300
	Ala Asn Ile Thr Leu Asn Thr Ala Asp Ile Ser Gln Pro Phe Glu Ile		
	305	310	315
45	Gly Leu Thr Arg Val Leu Pro Ser Gly Ser Trp Ala Tyr Ala Ala Ala		
	325	330	335
	Lys Phe Thr Val Glu Glu Tyr Asn Gln Tyr Ser Phe Leu Leu Lys Leu		
	340	345	350
50	Asn Lys Ala Ile Arg Leu Ser Arg Ala Thr Glu Leu Ser Pro Thr Ile		
	355	360	365
55	Leu Glu Gly Ile Val Arg Ser Val Asn Leu Gln Leu Asp Ile Asn Thr		
	370	375	380
	Asp Val Leu Gly Lys Val Phe Leu Thr Lys Tyr Tyr Met Gln Arg Tyr		
	385	390	395
60	Ala Ile His Ala Glu Thr Ala Leu Ile Leu Cys Asn Ala Pro Ile Ser		
	405	410	415
	Gln Arg Ser Tyr Asp Asn Gln Pro Ser Gln Phe Asp Arg Leu Phe Asn		
	420	425	430
65	Thr Pro Leu Leu Asn Gly Gln Tyr Phe Ser Thr Gly Asp Glu Glu Ile		
	435	440	445
70	Asp Leu Asn Ser Gly Ser Thr Gly Asp Trp Arg Lys Thr Ile Leu Lys		
	450	455	460

Arg Ala Phe Asn Ile Asp Asp Val Ser Leu Phe Arg Leu Leu Lys Ile
465 470 475 480

5 Thr Asp His Asp Asn Lys Asp Gly Lys Ile Lys Asn Asn Leu Lys Asn
485 490 495

Leu Ser Asn Leu Tyr Ile Gly Lys Leu Leu Ala Asp Ile His Gln Leu
500 505 510

10 Thr Ile Asp Glu Leu Asp Leu Leu Leu Ile Ala Val Gly Glu Gly Lys
515 520 525

Thr Asn Leu Ser Ala Ile Ser Asp Lys Gln Leu Ala Thr Leu Ile Arg
530 535 540

15 Lys Leu Asn Thr Ile Thr Ser Trp Leu His Thr Gln Lys Trp Ser Val
545 550 555 560

20 Phe Gln Leu Phe Ile Met Thr Ser Thr Ser Tyr Asn Lys Thr Leu Thr
565 570 575

Pro Glu Ile Lys Asn Leu Leu Asp Thr Val Tyr His Gly Leu Gln Gly
580 585 590

25 Phe Asp Lys Asp Lys Ala Asp Leu Leu His Val Met Ala Pro Tyr Ile
595 600 605

Ala Ala Thr Leu Gln Leu Ser Ser Glu Asn Val Ala His Ser Val Leu
610 615 620

30 Leu Trp Ala Asp Lys Leu Gln Pro Gly Asp Gly Ala Met Thr Ala Glu
625 630 635 640

35 Lys Phe Trp Asp Trp Leu Asn Thr Lys Tyr Thr Pro Gly Ser Ser Glu
645 650 655

Ala Val Glu Thr Gln Glu His Ile Val Gln Tyr Cys Gln Ala Leu Ala
660 665 670

40 Gln Leu Glu Met Val Tyr His Ser Thr Gly Ile Asn Glu Asn Ala Phe
675 680 685

Arg Leu Phe Val Thr Lys Pro Glu Met Phe Gly Ala Ala Thr Gly Ala
690 695 700

45 Ala Pro Ala His Asp Ala Leu Ser Leu Ile Met Leu Thr Arg Phe Ala
705 710 715 720

Asp Trp Val Asn Ala Leu Gly Glu Lys Ala Ser Ser Val Leu Ala Ala
725 730 735

50 Phe Glu Ala Asn Ser Leu Thr Ala Glu Gln Leu Ala Asp Ala Met Asn
740 745 750

55 Leu Asp Ala Asn Leu Leu Leu Gln Ala Ser Ile Gln Ala Gln Asn His
755 760 765

Gln His Leu Pro Pro Val Thr Pro Glu Asn Ala Phe Ser Cys Trp Thr
770 775 780

60 Ser Ile Asn Thr Ile Leu Gln Trp Val Asn Val Ala Gln Gln Leu Asn
785 790 795 800

Val Ala Pro Gln Gly Val Ser Ala Leu Val Gly Leu Asp Tyr Ile Gln
805 810 815

65 Ser Met Lys Glu Thr Pro Thr Tyr Ala Gln Trp Glu Asn Ala Ala Gly
820 825 830

Val Leu Thr Ala Gly Leu Asn Ser Gln Gln Ala Asn Thr Leu His Ala
835 840 845

70

	Phe	Leu	Asp	Glu	Ser	Arg	Ser	Ala	Ala	Leu	Ser	Thr	Tyr	Tyr	Ile	Arg	
	850						355					860					
5	Gln	Val	Ala	Lys	Ala	Ala	Ala	Ala	Ile	Lys	Ser	Arg	Asp	Asp	Leu	Tyr	
	365				370					875					880		
	Gln	Tyr	Leu	Leu	Ile	Asp	Asn	Gln	Val	Ser	Ala	Ala	Ile	Lys	Thr	Thr	
					885				890						895		
10	Arg	Ile	Ala	Glu	Ala	Ile	Ala	Ser	Ile	Gln	Leu	Tyr	Val	Asn	Arg	Ala	
				900					905					910			
	Leu	Glu	Asn	Val	Glu	Glu	Asn	Ala	Asn	Ser	Gly	Val	Ile	Ser	Arg	Gln	
			915					920					925				
15	Phe	Phe	Ile	Asp	Trp	Asp	Lys	Tyr	Asn	Lys	Arg	Tyr	Ser	Thr	Trp	Ala	
	930					935						940					
20	Gly	Val	Ser	Gln	Leu	Val	Tyr	Tyr	Pro	Glu	Asn	Tyr	Ile	Asp	Pro	Thr	
	945				950						955				960		
	Met	Arg	Ile	Gly	Gln	Thr	Lys	Met	Met	Asp	Ala	Leu	Leu	Gln	Ser	Val	
				965						970					975		
25	Ser	Gln	Ser	Gln	Leu	Asn	Ala	Asp	Thr	Val	Glu	Asp	Ala	Phe	Met	Ser	
				980					985					990			
	Tyr	Leu	Thr	Ser	Phe	Glu	Gln	Val	Ala	Asn	Leu	Lys	Val	Ile	Ser	Ala	
			995					1000					1005				
30	Tyr	His	Asp	Asn	Ile	Asn	Asn	Asp	Gln	Gly	Leu	Thr	Tyr	Phe	Ile	Gly	
	1010					1015						1020					
35	Leu	Ser	Glu	Thr	Asp	Ala	Gly	Glu	Tyr	Tyr	Trp	Arg	Ser	Val	Asp	His	
	1025					1030					1035				1040		
	Ser	Lys	Phe	Asn	Asp	Gly	Lys	Phe	Ala	Ala	Asn	Ala	Trp	Ser	Glu	Trp	
				1045						1050					1055		
40	His	Lys	Ile	Asp	Cys	Pro	Ile	Asn	Pro	Tyr	Lys	Ser	Thr	Ile	Arg	Pro	
				1060					1065					1070			
	Val	Ile	Tyr	Lys	Ser	Arg	Leu	Tyr	Leu	Leu	Trp	Leu	Glu	Gln	Lys	Glu	
			1075					1080					1085				
45	Ile	Thr	Lys	Gln	Thr	Gly	Asn	Ser	Lys	Asp	Gly	Tyr	Gln	Thr	Glu	Thr	
	1090					1095						1100					
50	Asp	Tyr	Arg	Tyr	Glu	Leu	Lys	Leu	Ala	His	Ile	Arg	Tyr	Asp	Gly	Thr	
	1105				1110						1115				1120		
	Trp	Asn	Thr	Pro	Ile	Thr	Phe	Asp	Val	Asn	Lys	Lys	Ile	Ser	Glu	Leu	
				1125					1130						1135		
55	Lys	Leu	Glu	Lys	Asn	Arg	Ala	Pro	Gly	Leu	Tyr	Cys	Ala	Gly	Tyr	Gln	
				1140					1145					1150			
	Gly	Glu	Asp	Thr	Leu	Leu	Val	Met	Phe	Tyr	Asn	Gln	Gln	Asp	Thr	Leu	
			1155					1160					1165				
60	Asp	Ser	Tyr	Lys	Asn	Ala	Ser	Met	Gln	Gly	Leu	Tyr	Ile	Phe	Ala	Asp	
	1170					1175						1180					
65	Met	Ala	Ser	Lys	Asp	Met	Thr	Pro	Glu	Gln	Ser	Asn	Val	Tyr	Arg	Asp	
	1185				1190						1195				1200		
	Asn	Ser	Tyr	Gln	Gln	Phe	Asp	Thr	Asn	Asn	Val	Arg	Arg	Val	Asn	Asn	
				1205					1210						1215		
70	Arg	Tyr	Ala	Glu	Asp	Tyr	Glu	Ile	Pro	Ser	Ser	Val	Ser	Ser	Arg	Lys	
				1220					1225						1230		

	Asp Tyr Gly Trp Gly Asp Tyr Tyr Leu Ser Met Val Tyr Asn Gly Asp	
	1235	1240 1245
5	Ile Pro Thr Ile Asn Tyr Lys Ala Ala Ser Ser Asp Leu Lys Ile Tyr	
	1250	1255 1260
	Ile Ser Pro Lys Leu Arg Ile Ile His Asn Gly Tyr Glu Gly Gln Lys	
	1255	1270 1275 1280
10	Arg Asn Gln Cys Asn Leu Met Asn Lys Tyr Gly Lys Leu Gly Asp Lys	
		1285 1290 1295
	Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn Ser Ser Asn	
15		1300 1305 1310
	Lys Leu Met Phe Tyr Pro Val Tyr Gln Tyr Ser Gly Asn Thr Ser Gly	
		1315 1320 1325
20	Leu Asn Gln Gly Arg Leu Leu Phe His Arg Asp Thr Thr Tyr Pro Ser	
		1330 1335 1340
	Lys Val Glu Ala Trp Ile Pro Gly Ala Lys Arg Ser Leu Thr Asn Gln	
	1345	1350 1355 1360
25	Asn Ala Ala Ile Gly Asp Asp Tyr Ala Thr Asp Ser Leu Asn Lys Pro	
		1365 1370 1375
	Asp Asp Leu Lys Gln Tyr Ile Phe Met Thr Asp Ser Lys Gly Thr Ala	
30		1380 1385 1390
	Thr Asp Val Ser Gly Pro Val Glu Ile Asn Thr Ala Ile Ser Pro Ala	
		1395 1400 1405
35	Lys Val Gln Ile Ile Val Lys Ala Gly Gly Lys Glu Gln Thr Phe Thr	
		1410 1415 1420
	Ala Asp Lys Asp Val Ser Ile Gln Pro Ser Pro Ser Phe Asp Glu Met	
	1425	1430 1435 1440
40	Asn Tyr Gln Phe Asn Ala Leu Glu Ile Asp Gly Ser Gly Leu Asn Phe	
		1445 1450 1455
	Ile Asn Asn Ser Ala Ser Ile Asp Val Thr Phe Thr Ala Phe Ala Glu	
45		1460 1465 1470
	Asp Gly Arg Lys Leu Gly Tyr Glu Ser Phe Ser Ile Pro Val Thr Leu	
		1475 1480 1485
50	Lys Val Ser Thr Asp Asn Ala Leu Thr Leu His His Asn Glu Asn Gly	
		1490 1495 1500
	Ala Gln Tyr Met Gln Trp Gln Ser Tyr Arg Thr Arg Leu Asn Thr Leu	
	1505	1510 1515 1520
55	Phe Ala Arg Gln Leu Val Ala Arg Ala Thr Thr Gly Ile Asp Thr Ile	
		1525 1530 1535
	Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu Gly Lys Gly	
60		1540 1545 1550
	Phe Tyr Ala Thr Phe Val Ile Pro Pro Tyr Asn Leu Ser Thr His Gly	
		1555 1560 1565
65	Asp Glu Arg Trp Phe Lys Leu Tyr Ile Lys His Val Val Asp Asn Asn	
		1570 1575 1580
	Ser His Ile Ile Tyr Ser Gly Gln Leu Thr Asp Thr Asn Ile Asn Ile	
	1585	1590 1595 1600
70	Thr Leu Phe Ile Pro Leu Asp Asp Val Pro Leu Asn Gln Asp Tyr His	

1605 1610 1615

Ala Lys Val Tyr Met Thr Phe Lys Lys Ser Pro Ser Asp Gly Thr Trp
1620 1625 1630

5 Trp Gly Pro His Phe Val Arg Asp Asp Lys Gly Ile Val Thr Ile Asn
1635 1640 1645

10 Pro Lys Ser Ile Leu Thr His Phe Glu Ser Val Asn Val Leu Asn Asn
1650 1655 1660

Ile Ser Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ser Leu Tyr Phe
1665 1670 1675 1680

15 Trp Glu Leu Phe Tyr Tyr Thr Pro Met Leu Val Ala Gln Arg Leu Leu
1685 1690 1695

His Glu Gln Asn Phe Asp Glu Ala Asn Arg Trp Leu Lys Tyr Val Trp
1700 1705 1710

20 Ser Pro Ser Gly Tyr Ile Val His Gly Gln Ile Gln Asn Tyr Gln Trp
1715 1720 1725

25 Asn Val Arg Pro Leu Leu Glu Asp Thr Ser Trp Asn Ser Asp Pro Leu
1730 1735 1740

Asp Ser Val Asp Pro Asp Ala Val Ala Gln His Asp Pro Met His Tyr
1745 1750 1755 1760

30 Lys Val Ser Thr Phe Met Arg Thr Leu Asp Leu Leu Ile Ala Arg Gly
1765 1770 1775

Asp His Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Asn Glu Ala Lys
1780 1785 1790

35 Met Trp Tyr Met Gln Ala Leu His Leu Leu Gly Asp Lys Pro Tyr Leu
1795 1800 1805

40 Pro Leu Ser Thr Thr Trp Ser Asp Pro Arg Leu Asp Arg Ala Ala Asp
1810 1815 1820

Ile Thr Thr Gln Asn Ala His Asp Ser Ala Ile Val Ala Leu Arg Gln
1825 1830 1835 1840

45 Asn Ile Pro Thr Pro Ala Pro Leu Ser
1845 1849

- (2) INFORMATION FOR SEQ ID NO:50:
- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 55 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50 (TcdA_{iii} coding region):

60 TTG CGC AGC GCT AAT ACC CTG ACT GAT CTC TTC CTG CCG CAA ATC AAT 48
Leu Arg Ser Ala Asn Thr Leu Thr Asp Leu Phe Leu Pro Gln Ile Asn
1 5 10 15

65 GAA GTG ATG ATG AAT TAC TGG CAG ACA TTA GCT CAG AGA GTA TAC AAT 96
Glu Val Met Met Asn Tyr Trp Gln Thr Leu Ala Gln Arg Val Tyr Asn
20 25 30

CTG CGT CAT AAC CTC TCT ATC GAC GGC CAG CCG TTA TAT CTG CCA ATC 144

	Leu	Arg	His	Asn	Leu	Ser	Ile	Asp	Gly	Gln	Pro	Leu	Tyr	Leu	Pro	Ile	
				35				40					45				
5	TAT	GCC	ACA	CCG	GCC	GAT	CCG	AAA	GCG	TTA	CTC	AGC	GCC	GCC	GTT	GCC	192
	Tyr	Ala	Thr	Pro	Ala	Asp	Pro	Lys	Ala	Leu	Leu	Ser	Ala	Ala	Val	Ala	
		50					55					60					
10	ACT	TCT	CAA	GGT	GGA	GGC	AAG	CTA	CCG	GAA	TCA	TTT	ATG	TCC	CTG	TGG	240
	Thr	Ser	Gln	Gly	Gly	Gly	Lys	Leu	Pro	Glu	Ser	Phe	Met	Ser	Leu	Trp	30
		55				70					75						
15	CGT	TTC	CCG	CAC	ATG	CTG	GAA	AAT	GCG	CGC	GGC	ATG	GTT	AGC	CAG	CTC	288
	Arg	Phe	Pro	His	Met	Leu	Glu	Asn	Ala	Arg	Gly	Met	Val	Ser	Gln	Leu	
				85					90						95		
20	ACC	CAG	TTC	GGC	TCC	ACG	TTA	CAA	AAT	ATT	ATC	GAA	CGT	CAG	GAC	GCG	336
	Thr	Gln	Phe	Gly	Ser	Thr	Leu	Gln	Asn	Ile	Ile	Glu	Arg	Gln	Asp	Ala	
				100					105					110			
25	GAA	GCG	CTC	AAT	GCG	TTA	TTA	CAA	AAT	CAG	GCC	GCC	GAG	CTG	ATA	TTG	384
	Glu	Ala	Leu	Asn	Ala	Leu	Leu	Gln	Asn	Gln	Ala	Ala	Glu	Leu	Ile	Leu	
				115				120					125				
30	ACT	AAC	CTG	AGC	ATT	CAG	GAC	AAA	ACC	ATT	GAA	GAA	TTG	GAT	GCC	GAG	432
	Thr	Asn	Leu	Ser	Ile	Gln	Asp	Lys	Thr	Ile	Glu	Glu	Leu	Asp	Ala	Glu	
		130					135					140					
35	AAA	ACG	GTG	TTG	GAA	AAA	TCC	AAA	GCG	GGA	GCA	CAA	TCG	CGC	TTT	GAT	480
	Lys	Thr	Val	Leu	Glu	Lys	Ser	Lys	Ala	Gly	Ala	Gln	Ser	Arg	Phe	Asp	160
		145				150				155							
40	AGC	TAC	GGC	AAA	CTG	TAC	GAT	GAG	AAT	ATC	AAC	GCC	GGT	GAA	AAC	CAA	528
	Ser	Tyr	Gly	Lys	Leu	Tyr	Asp	Glu	Asn	Ile	Asn	Ala	Gly	Glu	Asn	Gln	
				165					170					175			
45	GCC	ATG	ACG	CTA	CGA	GCG	TCC	GCC	GCC	GGG	CTT	ACC	ACG	GCA	GTT	CAG	576
	Ala	Met	Thr	Leu	Arg	Ala	Ser	Ala	Ala	Gly	Leu	Thr	Thr	Ala	Val	Gln	
				180				185					190				
50	GCA	TCC	CGT	CTG	GCC	GGT	GCG	GCG	GCT	GAT	CTG	GTG	CCT	AAC	ATC	TTC	624
	Ala	Ser	Arg	Leu	Ala	Gly	Ala	Ala	Ala	Asp	Leu	Val	Pro	Asn	Ile	Phe	
			195				200					205					
55	GGC	TTT	GCC	GGT	GGC	GGC	AGC	CGT	TGG	GGG	GCT	ATC	GCT	GAG	GCG	ACA	672
	Gly	Phe	Ala	Gly	Gly	Gly	Ser	Arg	Trp	Gly	Ala	Ile	Ala	Glu	Ala	Thr	
		210				215					220						
60	GGT	TAT	GTG	ATG	GAA	TTC	TCC	GCG	AAT	GTT	ATG	AAC	ACC	GAA	GCG	GAT	720
	Gly	Tyr	Val	Met	Glu	Phe	Ser	Ala	Asn	Val	Met	Asn	Thr	Glu	Ala	Asp	240
		225				230					235						
65	AAA	ATT	AGC	CAA	TCT	GAA	ACC	TAC	CGT	CGT	CGC	CGT	CAG	GAG	TGG	GAG	768
	Lys	Ile	Ser	Gln	Ser	Glu	Thr	Tyr	Arg	Arg	Arg	Arg	Gln	Glu	Trp	Glu	
				245					250					255			
70	ATC	CAG	CGG	AAT	AAT	GCC	GAA	GCG	GAA	TTG	AAG	CAA	ATC	GAT	GCT	CAG	816
	Ile	Gln	Arg	Asn	Asn	Ala	Glu	Ala	Glu	Leu	Lys	Gln	Ile	Asp	Ala	Gln	
				260				265					270				
75	CTC	AAA	TCA	CTC	GCT	GTA	CGC	CGC	GAA	GCC	GCC	GTA	TTG	CAG	AAA	ACC	864
	Leu	Lys	Ser	Leu	Ala	Val	Arg	Arg	Glu	Ala	Ala	Val	Leu	Gln	Lys	Thr	
				275			280					285					
80	AGT	CTG	AAA	ACC	CAA	CAA	GAA	CAG	ACC	CAA	TCT	CAA	TTG	GCC	TTC	CTG	912
	Ser	Leu	Lys	Thr	Gln	Gln	Glu	Gln	Thr	Gln	Ser	Gln	Leu	Ala	Phe	Leu	
		290				295					300						
85	CAA	CGT	AAG	TTC	AGC	AAT	CAG	GCG	TTA	TAC	AAC	TGG	CTG	CGT	CGT	CGA	960
	Gln	Arg	Lys	Phe	Ser	Asn	Gln	Ala	Leu	Tyr	Asn	Trp	Leu	Arg	Gly	Arg	
		305				310				315						320	

CTG GCG GCG ATT TAC TTC CAG TTC TAC GAT TTG GCC CTC GCG CGT TGC 1008
 Leu Ala Ala Ile Tyr Phe Gln Phe Tyr Asp Leu Ala Val Ala Arg Cys
 325 330 335

5 CTG ATG GCA GAA CAA GCT TAC CGT TGG GAA CTC AAT GAT GAC TCT GCC 1056
 Leu Met Ala Glu Gln Ala Tyr Arg Trp Glu Leu Asn Asp Asp Ser Ala
 340 345 350

10 CGC TTC ATT AAA CCG GGC GCC TGG CAG GGA ACC TAT GCC GGT CTG CTT 1104
 Arg Phe Ile Lys Pro Gly Ala Trp Gln Gly Thr Tyr Ala Gly Leu Leu
 355 360 365

15 GCA GGT GAA ACC TTG ATG CTG AGT CTG GCA CAA ATG GAA GAC GCT CAT 1152
 Ala Gly Glu Thr Leu Met Leu Ser Leu Ala Gln Met Glu Asp Ala His
 370 375 380

20 CTG AAA CGC GAT AAA CGC GCA TTA GAG GTT GAA CGC ACA GTA TCG CTG 1200
 Leu Lys Arg Asp Lys Arg Ala Leu Glu Val Glu Arg Thr Val Ser Leu
 385 390 395 400

GCC GAA GTT TAT GCA GGA TTA CCA AAA GAT AAC GGT CCA TTT TCC CTG 1248
 Ala Glu Val Tyr Ala Gly Leu Pro Lys Asp Asn Gly Pro Phe Ser Leu
 405 410 415

25 GCT CAG GAA ATT GAC AAG CTG GTG AGT CAA GGT TCA GGC AGT GCC GGC 1296
 Ala Gln Glu Ile Asp Lys Leu Val Ser Gln Gly Ser Gly Ser Ala Gly
 420 425 430

30 AGT GGT AAT AAT AAT TTG GCG TTC GGC GCC GGC ACG GAC ACT AAA ACC 1344
 Ser Gly Asn Asn Asn Leu Ala Phe Gly Ala Gly Thr Asp Thr Lys Thr
 435 440 445

35 TCT TTG CAG GCA TCA GTT TCA TTC GCT GAT TTG AAA ATT CGT GAA GAT 1392
 Ser Leu Gln Ala Ser Val Ser Phe Ala Asp Leu Lys Ile Arg Glu Asp
 450 455 460

40 TAC CCG GCA TCG CTT GGC AAA ATT CGA CGT ATC AAA CAG ATC AGC GTC 1440
 Tyr Pro Ala Ser Leu Gly Lys Ile Arg Arg Ile Lys Gln Ile Ser Val
 465 470 475 480

ACT TTG CCC GCG CTA CTG GGA CCG TAT CAG GAT GTA CAG GCA ATA TTG 1488
 Thr Leu Pro Ala Leu Leu Gly Pro Tyr Gln Asp Val Gln Ala Ile Leu
 485 490 495

45 TCT TAC GGC GAT AAA GCC GGA TTA GCT AAC GGC TGT GAA GCG CTG GCA 1536
 Ser Tyr Gly Asp Lys Ala Gly Leu Ala Asn Gly Cys Glu Ala Leu Ala
 500 505 510

50 GTT TCT CAC GGT ATG AAT GAC AGC GGC CAA TTC CAG CTC GAT TTC AAC 1584
 Val Ser His Gly Met Asn Asp Ser Gly Gln Phe Gln Leu Asp Phe Asn
 515 520 525

55 GAT GGC AAA TTC CTG CCA TTC GAA GGC ATC GCC ATT GAT CAA GGC ACG 1632
 Asp Gly Lys Phe Leu Pro Phe Glu Gly Ile Ala Ile Asp Gln Gly Thr
 530 535 540

60 CTG ACA CTG AGC TTC CCA AAT GCA TCT ATG CCG GAG AAA GGT AAA CAA 1680
 Leu Thr Leu Ser Phe Pro Asn Ala Ser Met Pro Glu Lys Gly Lys Gln
 545 550 555 560

GCC ACT ATG TTA AAA ACC CTG AAC GAT ATC ATT TTG CAT ATT CGC TAC 1728
 Ala Thr Met Leu Lys Thr Leu Asn Asp Ile Ile Leu His Ile Arg Tyr
 565 570 575

65 ACC ATT AAA TAA 1740
 Thr Ile Lys ...
 579

70 (2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 579 amino acids
 (B) TYPE: amino acids
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51 (TcdAiii):

10	Leu Arg Ser Ala Asn Thr Leu Thr Asp Leu Phe Leu Pro Gln Ile Asn	1	5	10	15
15	Glu Val Met Met Asn Tyr Trp Gln Thr Leu Ala Gln Arg Val Tyr Asn	20	25	30	
	Leu Arg His Asn Leu Ser Ile Asp Gly Gln Pro Leu Tyr Leu Pro Ile	35	40	45	
20	Tyr Ala Thr Pro Ala Asp Pro Lys Ala Leu Leu Ser Ala Ala Val Ala	50	55	60	
	Thr Ser Gln Gly Gly Gly Lys Leu Pro Glu Ser Phe Met Ser Leu Trp	65	70	75	80
25	Arg Phe Pro His Met Leu Glu Asn Ala Arg Gly Met Val Ser Gln Leu	85	90	95	
	Thr Gln Phe Gly Ser Thr Leu Gln Asn Ile Ile Glu Arg Gln Asp Ala	100	105	110	
30	Glu Ala Leu Asn Ala Leu Leu Gln Asn Gln Ala Ala Glu Leu Ile Leu	115	120	125	
	Thr Asn Leu Ser Ile Gln Asp Lys Thr Ile Glu Glu Leu Asp Ala Glu	130	135	140	
	Lys Thr Val Leu Glu Lys Ser Lys Ala Gly Ala Gln Ser Arg Phe Asp	145	150	155	160
40	Ser Tyr Gly Lys Leu Tyr Asp Glu Asn Ile Asn Ala Gly Glu Asn Gln	165	170	175	
	Ala Met Thr Leu Arg Ala Ser Ala Ala Gly Leu Thr Thr Ala Val Gln	180	185	190	
45	Ala Ser Arg Leu Ala Gly Ala Ala Ala Asp Leu Val Pro Asn Ile Phe	195	200	205	
	Gly Phe Ala Gly Gly Gly Ser Arg Trp Gly Ala Ile Ala Glu Ala Thr	210	215	220	
	Gly Tyr Val Met Glu Phe Ser Ala Asn Val Met Asn Thr Glu Ala Asp	225	230	235	240
55	Lys Ile Ser Gln Ser Glu Thr Tyr Arg Arg Arg Arg Gln Glu Trp Glu	245	250	255	
	Ile Gln Arg Asn Asn Ala Glu Ala Glu Leu Lys Gln Ile Asp Ala Gln	260	265	270	
60	Leu Lys Ser Leu Ala Val Arg Arg Glu Ala Ala Val Leu Gln Lys Thr	275	280	285	
	Ser Leu Lys Thr Gln Gln Glu Gln Thr Gln Ser Gln Leu Ala Phe Leu	290	295	300	
65	Gln Arg Lys Phe Ser Asn Gln Ala Leu Tyr Asn Trp Leu Arg Gly Arg	305	310	315	320

Leu Ala Ala Ile Tyr Phe Gln Phe Tyr Asp Leu Ala Val Ala Arg Cys
 325 330 335
 5 Leu Met Ala Glu Gln Ala Tyr Arg Trp Glu Leu Asn Asp Asp Ser Ala
 340 345 350
 Arg Phe Ile Lys Pro Gly Ala Trp Gln Gly Thr Tyr Ala Gly Leu Leu
 355 360 365
 10 Ala Gly Glu Thr Leu Met Leu Ser Leu Ala Gln Met Glu Asp Ala His
 370 375 380
 Leu Lys Arg Asp Lys Arg Ala Leu Glu Val Glu Arg Thr Val Ser Leu
 385 390 395 400
 15 Ala Glu Val Tyr Ala Gly Leu Pro Lys Asp Asn Gly Pro Phe Ser Leu
 405 410 415
 20 Ala Gln Glu Ile Asp Lys Leu Val Ser Gln Gly Ser Gly Ser Ala Gly
 420 425 430
 Ser Gly Asn Asn Asn Leu Ala Phe Gly Ala Gly Thr Asp Thr Lys Thr
 435 440 445
 25 Ser Leu Gln Ala Ser Val Ser Phe Ala Asp Leu Lys Ile Arg Glu Asp
 450 455 460
 Tyr Pro Ala Ser Leu Gly Lys Ile Arg Arg Ile Lys Gln Ile Ser Val
 465 470 475 480
 30 Thr Leu Pro Ala Leu Leu Gly Pro Tyr Gln Asp Val Gln Ala Ile Leu
 485 490 495
 35 Ser Tyr Gly Asp Lys Ala Gly Leu Ala Asn Gly Cys Glu Ala Leu Ala
 500 505 510
 Val Ser His Gly Met Asn Asp Ser Gly Gln Phe Gln Leu Asp Phe Asn
 515 520 525
 40 Asp Gly Lys Phe Leu Pro Phe Glu Gly Ile Ala Ile Asp Gln Gly Thr
 530 535 540
 Leu Thr Leu Ser Phe Pro Asn Ala Ser Met Pro Glu Lys Gly Lys Gln
 545 550 555 560
 45 Ala Thr Met Leu Lys Thr Leu Asn Asp Ile Ile Leu His Ile Arg Tyr
 565 570 575
 50 Thr Ile Lys ...
 579

(2) INFORMATION FOR SEQ ID NO:52:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5532 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52 (TcdA_{iii} coding region):

65 TTT ATA CAA GGT TAT AGT GAT CTG TTT GGT AAT CCT GCT GAT AAC TAT 48
 Phe Ile Gln Gly Tyr Ser Asp Leu Phe Gly Asn Arg Ala Asp Asn Tyr
 1 5 10 15
 GCC GCG CCG GGC TCG GTT GCA TCG ATG TTC TCA CCG GCG GCT TAT TTG 96

	Ala	Ala	Pro	Gly	Ser	Val	Ala	Ser	Met	Phe	Ser	Pro	Ala	Ala	Tyr	Leu	
				20					25					30			
5	ACG	GAA	TTG	TAC	CGT	GAA	GCC	AAA	AAC	TTG	CAT	GAC	AGC	AGC	TCA	ATT	144
	Thr	Glu	Leu	Tyr	Arg	Glu	Ala	Lys	Asn	Leu	His	Asp	Ser	Ser	Ser	Ile	
			35					40					45				
10	TAT	TAC	CTA	GAT	AAA	CGT	CGC	CCG	GAT	TTA	GCA	AGC	TTA	ATG	CTC	AGC	192
	Tyr	Tyr	Leu	Asp	Lys	Arg	Arg	Pro	Asp	Leu	Ala	Ser	Leu	Met	Leu	Ser	
			50				55					60					
15	CAG	AAA	AAT	ATC	GAT	GAG	GAA	ATT	TCA	ACG	CTG	GCT	CTC	TCT	AAT	GAA	240
	Gln	Lys	Asn	Met	Asp	Glu	Glu	Ile	Ser	Thr	Leu	Ala	Leu	Ser	Asn	Glu	
	65					70				75						80	
	TTG	TGC	CTT	GCC	GGG	ATC	GAA	ACA	AAA	ACA	GGA	AAA	TCA	CAA	GAT	GAA	288
	Leu	Cys	Leu	Ala	Gly	Ile	Glu	Thr	Lys	Thr	Gly	Lys	Ser	Gln	Asp	Glu	
					85			90							95		
20	GTG	ATG	GAT	ATC	TTG	TCA	ACT	TAT	CGT	TTA	AGT	GGA	GAG	ACA	CCT	TAT	336
	Val	Met	Asp	Met	Leu	Ser	Thr	Tyr	Arg	Leu	Ser	Gly	Glu	Thr	Pro	Tyr	
				100					105					110			
25	CAT	CAC	GCT	TAT	GAA	ACT	GTT	CGT	GAA	ATC	GTT	CAT	GAA	CGT	GAT	CCA	384
	His	His	Ala	Tyr	Glu	Thr	Val	Arg	Glu	Ile	Val	His	Glu	Arg	Asp	Pro	
			115					120					125				
30	GGA	TTT	CGT	CAT	TTG	TCA	CAG	GCA	CCC	ATT	GTT	GCT	GCT	AAG	CTC	GAT	432
	Gly	Phe	Arg	His	Leu	Ser	Gln	Ala	Pro	Ile	Val	Ala	Ala	Lys	Leu	Asp	
		130					135					140					
35	CCT	GTG	ACT	TTG	TTG	GGT	ATT	AGC	TCC	CAT	ATT	TCG	CCA	GAA	CTG	TAT	480
	Pro	Val	Thr	Leu	Leu	Gly	Ile	Ser	Ser	His	Ile	Ser	Pro	Glu	Leu	Tyr	
	145					150					155					160	
	AAC	TTG	CTG	ATT	GAG	GAG	ATC	CCG	GAA	AAA	GAT	GAA	GCC	GCG	CTT	GAT	528
	Asn	Leu	Leu	Ile	Glu	Glu	Ile	Pro	Glu	Lys	Asp	Glu	Ala	Ala	Leu	Asp	
					165				170						175		
40	ACG	CTT	TAT	AAA	ACA	AAC	TTT	GGC	GAT	ATT	ACT	ACT	GCT	CAG	TTA	ATG	576
	Thr	Leu	Tyr	Lys	Thr	Asn	Phe	Gly	Asp	Ile	Thr	Thr	Ala	Gln	Leu	Met	
				180					185					190			
45	TCC	CCA	AGT	TAT	CTG	GCC	CGG	TAT	TAT	GGC	GTC	TCA	CCG	GAA	GAT	ATT	624
	Ser	Pro	Ser	Tyr	Leu	Ala	Arg	Tyr	Tyr	Gly	Val	Ser	Pro	Glu	Asp	Ile	
			195					200					205				
50	GCC	TAC	GTG	ACG	ACT	TCA	TTA	TCA	CAT	GTT	GGA	TAT	AGC	AGT	GAT	ATT	672
	Ala	Tyr	Val	Thr	Thr	Ser	Leu	Ser	His	Val	Gly	Tyr	Ser	Ser	Asp	Ile	
		210					215					220					
55	CTG	GTT	ATT	CCG	TTG	GTC	GAT	GGT	GTG	GGT	AAG	ATG	GAA	GTA	GTT	CGT	720
	Leu	Val	Ile	Pro	Leu	Val	Asp	Gly	Val	Gly	Lys	Met	Glu	Val	Val	Arg	
	225					230					235					240	
	GTT	ACC	CGA	ACA	CCA	TCG	GAT	AAT	TAT	ACC	AGT	CAG	ACG	AAT	TAT	ATT	768
	Val	Thr	Arg	Thr	Pro	Ser	Asp	Asn	Tyr	Thr	Ser	Gln	Thr	Asn	Tyr	Ile	
					245				250						255		
60	GAG	CTG	TAT	CCA	CAG	GGT	GGC	GAC	AAT	TAT	TTG	ATC	AAA	TAC	AAT	CTA	816
	Glu	Leu	Tyr	Pro	Gln	Gly	Gly	Asp	Asn	Tyr	Leu	Ile	Lys	Tyr	Asn	Leu	
				260					265					270			
65	AGC	AAT	AGT	TTT	GGT	TTG	GAT	GAT	TTT	TAT	CTG	CAA	TAT	AAA	GAT	GGT	864
	Ser	Asn	Ser	Phe	Gly	Leu	Asp	Asp	Phe	Tyr	Leu	Gln	Tyr	Lys	Asp	Gly	
			275					280					285				
70	TCC	GCT	GAT	TGG	ACT	GAG	ATT	GCC	CAT	AAT	CCC	TAT	CCT	GAT	ATG	GTC	912
	Ser	Ala	Asp	Trp	Thr	Glu	Ile	Ala	His	Asn	Pro	Tyr	Pro	Asp	Met	Val	
		290					295					300					

	ATA	AAT	CAA	AAG	TAT	GAA	TCA	CAG	GCG	ACA	ATC	AAA	CGT	AGT	GAC	TTT	350
	Ile	Asn	Gln	Lys	Tyr	Glu	Ser	Gln	Ala	Thr	Ile	Lys	Arg	Ser	Asp	Ser	320
	305					310					315						
5	EAC	AAT	ATA	CTC	AGT	ATA	GGG	TTA	CAA	AGA	TGG	CAT	AGC	GGT	AGT	TAT	1008
	Asp	Asn	Ile	Leu	Ser	Ile	Gly	Leu	Gln	Arg	Trp	His	Ser	Gly	Ser	Tyr	
					325					330					335		
10	AAT	TTT	GCC	GCC	GCC	AAT	TTT	AAA	ATT	GAC	CAA	TAC	TCC	CCG	AAA	GCT	1056
	Asn	Phe	Ala	Ala	Ala	Asn	Phe	Lys	Ile	Asp	Gln	Tyr	Ser	Pro	Lys	Ala	
					340					345				350			
15	TTC	CTG	CTT	AAA	ATG	AAT	AAG	GCT	ATT	CGG	TTG	CTC	AAA	GCT	ACC	GGC	1104
	Phe	Leu	Leu	Lys	Met	Asn	Lys	Ala	Ile	Arg	Leu	Leu	Lys	Ala	Thr	Gly	
				355				360					365				
20	CTC	TCT	TTT	GCT	ACG	TTG	GAG	CGT	ATT	GTT	GAT	AGT	GTT	AAT	AGC	ACC	1152
	Leu	Ser	Phe	Ala	Thr	Leu	Glu	Arg	Ile	Val	Asp	Ser	Val	Asn	Ser	Thr	
		370					375				380						
25	AAA	TCC	ATC	ACG	GTT	GAG	GTA	TTA	AAC	AAG	GTT	TAT	CGG	GTA	AAA	TTC	1200
	Lys	Ser	Ile	Thr	Val	Glu	Val	Leu	Asn	Lys	Val	Tyr	Arg	Val	Lys	Phe	
	385					390					395				400		
30	TAT	ATT	GAT	CGT	TAT	GGC	ATC	AGT	GAA	GAG	ACA	GCC	GCT	ATT	TTG	GCT	1248
	Tyr	Ile	Asp	Arg	Tyr	Gly	Ile	Ser	Glu	Glu	Thr	Ala	Ala	Ile	Leu	Ala	
					405					410					415		
35	AAT	ATT	AAT	ATC	TCT	CAG	CAA	GCT	GTT	GGC	AAT	CAG	CTT	AGC	CAG	TTT	1296
	Asn	Ile	Asn	Ile	Ser	Gln	Gln	Ala	Val	Gly	Asn	Gln	Leu	Ser	Gln	Phe	
				420					425					430			
40	GAG	CAA	CTA	TTT	AAT	CAC	CCG	CCG	CTC	AAT	GGT	ATT	CGC	TAT	GAA	ATC	1344
	Glu	Gln	Leu	Phe	Asn	His	Pro	Pro	Leu	Asn	Gly	Ile	Arg	Tyr	Glu	Ile	
			435					440					445				
45	AGT	GAG	GAC	AAC	TCC	AAA	CAT	CTT	CCT	AAT	CCT	GAT	CTG	AAC	CTT	AAA	1392
	Ser	Glu	Asp	Asn	Ser	Lys	His	Leu	Pro	Asn	Pro	Asp	Leu	Asn	Leu	Lys	
		450					455					460					
50	CCA	GAC	AGT	ACC	GGT	GAT	GAT	CAA	CGC	AAG	GCG	GTT	TTA	AAA	CGC	GCG	1440
	Pro	Asp	Ser	Thr	Gly	Asp	Asp	Gln	Arg	Lys	Ala	Val	Leu	Lys	Arg	Ala	
	465					470					475				480		
55	TTT	CAG	GTT	AAC	GCC	AGT	GAG	TTG	TAT	CAG	ATG	TTA	TTG	ATC	ACT	GAT	1488
	Phe	Gln	Val	Asn	Ala	Ser	Glu	Leu	Tyr	Gln	Met	Leu	Leu	Ile	Thr	Asp	
					485					490					495		
60	CGT	AAA	GAA	GAC	GGT	GTT	ATC	AAA	AAT	AAC	TTA	GAG	AAT	TTG	TCT	GAT	1536
	Arg	Lys	Glu	Asp	Gly	Val	Ile	Lys	Asn	Asn	Leu	Glu	Asn	Leu	Ser	Asp	
				500					505					510			
65	CTG	TAT	TTG	GTT	AGT	TTG	CTG	GCC	CAG	ATT	CAT	AAC	CTG	ACT	ATT	GCT	1584
	Leu	Tyr	Leu	Val	Ser	Leu	Leu	Ala	Gln	Ile	His	Asn	Leu	Thr	Ile	Ala	
			515					520					525				
70	GAA	TTG	AAC	ATT	TTG	TTG	GTG	ATT	TGT	GGC	TAT	GGC	GAC	ACC	AAC	ATT	1632
	Glu	Leu	Asn	Ile	Leu	Leu	Val	Ile	Cys	Gly	Tyr	Gly	Asp	Thr	Asn	Ile	
		530					535				540						
75	TAT	CAG	ATT	ACC	GAC	GAT	AAT	TTA	GCC	AAA	ATA	GTG	GAA	ACA	TTG	TTG	1680
	Tyr	Gln	Ile	Thr	Asp	Asp	Asn	Leu	Ala	Lys	Ile	Val	Glu	Thr	Leu	Leu	
	545					550					555				560		
80	TGG	ATC	ACT	CAA	TGG	TTG	AAG	ACC	CAA	AAA	TGG	ACA	GTT	ACC	GAC	CTG	1728
	Trp	Ile	Thr	Gln	Trp	Leu	Lys	Thr	Gln	Lys	Trp	Thr	Val	Thr	Asp	Leu	
					565					570					575		
85	TTT	CTG	ATG	ACC	ACG	GCC	ACT	TAC	AGC	ACC	ACT	TTA	ACG	CCA	GAA	ATT	1776
	Phe	Leu	Met	Thr	Thr	Ala	Thr	Tyr	Ser	Thr	Thr	Leu	Thr	Pro	Glu	Ile	
				580					585					590			

AGC AAT CTG ACG GCT ACG TTG TCT TCA ACT TTG CAT GGC AAA GAG AGT 1824
 Ser Asn Leu Thr Ala Thr Leu Ser Ser Thr Leu His Gly Lys Glu Ser
 595 600 605
 5 CTG ATT GGG GAA GAT CTG AAA AGA GCA ATG GCG CCT TGC TTC ACT TCG 1872
 Leu Ile Gly Glu Asp Leu Lys Arg Ala Met Ala Pro Cys Phe Thr Ser
 610 615 620
 10 GCT TTG CAT TTG ACT TCT CAA GAA GTT GCG TAT GAC CTG CTG TTG TGG 1920
 Ala Leu His Leu Thr Ser Gln Glu Val Ala Tyr Asp Leu Leu Leu Trp
 625 630 635 640
 15 ATA GAC CAG ATT CAA CCG GCA CAA ATA ACT GTT GAT GGG TTT TCG GAA 1968
 Ile Asp Gln Ile Gln Pro Ala Gln Ile Thr Val Asp Gly Phe Trp Glu
 645 650 655
 20 GAA GTG CAA ACA ACA CCA ACC AGC TTG AAG GTG ATT ACC TTT GCT CAG 2016
 Glu Val Gln Thr Thr Pro Thr Ser Leu Lys Val Ile Thr Phe Ala Gln
 660 665 670
 25 GTG CTG GCA CAA TTG AGC CTG ATC TAT CGT CGT ATT GGG TTA AGT GAA 2064
 Val Leu Ala Gln Leu Ser Leu Ile Tyr Arg Arg Ile Gly Leu Ser Glu
 675 680 685
 ACG GAA CTG TCA CTG ATC GTG ACT CAA TCT TCT CTG CTA GTG GCA GGC 2112
 Thr Glu Leu Ser Leu Ile Val Thr Gln Ser Ser Leu Leu Val Ala Gly
 690 695 700
 30 AAA AGC ATA CTG GAT CAC GGT CTG TTA ACC CTG ATG GCC TTG GAA GGT 2160
 Lys Ser Ile Leu Asp His Gly Leu Leu Thr Leu Met Ala Leu Glu Gly
 705 710 715 720
 35 TTT CAT ACC TGG GTT AAT GGC TTG GGG CAA CAT GCC TCC TTG ATA TTG 2208
 Phe His Thr Trp Val Asn Gly Leu Gly Gln His Ala Ser Leu Ile Leu
 725 730 735
 40 GCG GCG TTG AAA GAC GGA GCC TTG ACA GTT ACC GAT GTA GCA CAA GCT 2256
 Ala Ala Leu Lys Asp Gly Ala Leu Thr Val Thr Asp Val Ala Gln Ala
 740 745 750
 45 ATG AAT AAG GAG GAA TCT CTC CTA CAA ATG GCA GCT AAT CAG GTG GAG 2304
 Met Asn Lys Glu Glu Ser Leu Leu Gln Met Ala Ala Asn Gln Val Glu
 755 760 765
 AAG GAT CTA ACA AAA CTG ACC AGT TGG ACA CAG ATT GAC GCT ATT CTG 2352
 Lys Asp Leu Thr Lys Leu Thr Ser Trp Thr Gln Ile Asp Ala Ile Leu
 770 775 780
 50 CAA TGG TTA CAG ATG TCT TCG GCC TTG GCG GTT TCT CCA CTG GAT CTG 2400
 Gln Trp Leu Gln Met Ser Ser Ala Leu Ala Val Ser Pro Leu Asp Leu
 785 790 795 800
 55 GCA GGG ATG ATG GCC CTG AAA TAT GGG ATA GAT CAT AAC TAT GCT GCC 2448
 Ala Gly Met Met Ala Leu Lys Tyr Gly Ile Asp His Asn Tyr Ala Ala
 805 810 815
 60 TGG CAA GCT GCG GCG GCT GCG CTG ATG GCT GAT CAT GCT AAT CAG GCA 2496
 Trp Gln Ala Ala Ala Ala Leu Met Ala Asp His Ala Asn Gln Ala
 820 825 830
 65 CAG AAA AAA CTG GAT GAG ACG TTC AGT AAG GCA TTA TGT AAC TAT TAT 2544
 Gln Lys Lys Leu Asp Glu Thr Phe Ser Lys Ala Leu Cys Asn Tyr Tyr
 835 840 845
 ATT AAT GCT GTT GTC GAT AGT GCT GCT GGA GTA CGT GAT CGT AAC GGT 2592
 Ile Asn Ala Val Val Asp Ser Ala Ala Gly Val Arg Asp Arg Asn Gly
 850 855 860
 70 TTA TAT ACC TAT TTG CTG ATT GAT AAT CAG GTT TCT GCC GAT GTG ATC 2640
 Leu Tyr Thr Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Asp Val Ile

	365			370				375					380				
5	ACT	TCA	CGT	ATT	GCA	GAA	GCT	ATC	GCC	GGT	ATT	CAA	CTG	TAC	GTT	AAC	2688
	Thr	Ser	Arg	Ile	Ala	Glu	Ala	Ile	Ala	Gly	Ile	Gln	Leu	Tyr	Val	Asn	
					885					890					895		
10	CGG	GCT	TTA	AAC	CGA	GAT	GAA	GGT	CAG	CTT	GCA	TCG	GAC	GTT	AGT	ACC	2736
	Arg	Ala	Leu	Asn	Arg	Asp	Glu	Gly	Gln	Leu	Ala	Ser	Asp	Val	Ser	Thr	
				900					905					910			
15	CGT	CAG	TTC	TTC	ACT	GAC	TGG	GAA	CGT	TAC	AAT	AAA	CGT	TAC	AGT	ACT	2784
	Arg	Gln	Phe	Phe	Thr	Asp	Trp	Glu	Arg	Tyr	Asn	Lys	Arg	Tyr	Ser	Thr	
			915					920					925				
20	TGG	GCT	GGT	GTC	TCT	GAA	CTG	GTC	TAT	TAT	CCA	GAA	AAC	TAT	GTT	GAT	2832
	Trp	Ala	Gly	Val	Ser	Glu	Leu	Val	Tyr	Tyr	Pro	Glu	Asn	Tyr	Val	Asp	
		930					935					940					
25	CCC	ACT	CAG	CGC	ATT	GGG	CAA	ACC	AAA	ATG	ATG	GAT	GCG	CTG	TTG	CAA	2880
	Pro	Thr	Gln	Arg	Ile	Gly	Gln	Thr	Lys	Met	Met	Asp	Ala	Leu	Leu	Gln	
	945					950				955					960		
30	TCC	ATC	AAC	CAG	AGC	CAG	CTA	AAT	GCG	GAT	ACG	GTG	GAA	GAT	GCT	TTC	2928
	Ser	Ile	Asn	Gln	Ser	Gln	Leu	Asn	Ala	Asp	Thr	Val	Glu	Asp	Ala	Phe	
					965				970						975		
35	AAA	ACT	TAT	TTG	ACC	AGC	TTT	GAG	CAG	GTA	GCA	AAT	CTG	AAA	GTA	ATT	2976
	Lys	Thr	Tyr	Leu	Thr	Ser	Phe	Glu	Gln	Val	Ala	Asn	Leu	Lys	Val	Ile	
				980				985					990				
40	AGT	GCT	TAC	CAC	GAT	AAT	GTG	AAT	GTG	GAT	CAA	GGA	TTA	ACT	TAT	TTT	3024
	Ser	Ala	Tyr	His	Asp	Asn	Val	Asn	Val	Asp	Gln	Gly	Leu	Thr	Tyr	Phe	
			995				1000					1005					
45	ATC	GGT	ATC	GAC	CAA	GCA	GCT	CCG	GGT	ACG	TAT	TAC	TGG	CGT	AGT	GTT	3072
	Ile	Gly	Ile	Asp	Gln	Ala	Ala	Pro	Gly	Thr	Tyr	Tyr	Trp	Arg	Ser	Val	
		1010					1015					1020					
50	GAT	CAC	AGC	AAA	TGT	GAA	AAT	GGC	AAG	TTT	GCC	GCT	AAT	GCT	TGG	GGT	3120
	Asp	His	Ser	Lys	Cys	Glu	Asn	Gly	Lys	Phe	Ala	Ala	Asn	Ala	Trp	Gly	
	1025					1030				1035					1040		
55	GAG	TGG	AAT	AAA	ATT	ACC	TGT	GCT	GTC	AAT	CCT	TGG	AAA	AAT	ATC	ATC	3168
	Glu	Trp	Asn	Lys	Ile	Thr	Cys	Ala	Val	Asn	Pro	Trp	Lys	Asn	Ile	Ile	
					1045					1050					1055		
60	CGT	CCG	GTT	GTT	TAT	ATG	TCC	CGC	TTA	TAT	CTG	CTA	TGG	CTG	GAG	CAG	3216
	Arg	Pro	Val	Val	Tyr	Met	Ser	Arg	Leu	Tyr	Leu	Leu	Trp	Leu	Glu	Gln	
				1060					1065				1070				
65	CAA	TCA	AAG	AAA	AGT	GAT	GAT	GGT	AAA	ACC	ACG	ATT	TAT	CAA	TAT	AAC	3264
	Gln	Ser	Lys	Lys	Ser	Asp	Asp	Gly	Lys	Thr	Thr	Ile	Tyr	Gln	Tyr	Asn	
			1075					1080				1085					
70	TTA	AAA	CTG	GCT	CAT	ATT	CGT	TAC	GAC	GGT	AGT	TGG	AAT	ACA	CCA	TTT	3312
	Leu	Lys	Leu	Ala	His	Ile	Arg	Tyr	Asp	Gly	Ser	Trp	Asn	Thr	Pro	Phe	
			1090				1095					1100					
75	ACT	TTT	GAT	GTG	ACA	GAA	AAG	GTA	AAA	AAT	TAC	ACG	TCG	AGT	ACT	GAT	3360
	Thr	Phe	Asp	Val	Thr	Glu	Lys	Val	Lys	Asn	Tyr	Thr	Ser	Ser	Thr	Asp	
	1105					1110				1115					1120		
80	GCT	GCT	GAA	TCT	TTA	GGG	TTG	TAT	TGT	ACT	GGT	TAT	CAA	GGG	GAA	GAC	3408
	Ala	Ala	Glu	Ser	Leu	Gly	Leu	Tyr	Cys	Thr	Gly	Tyr	Gln	Gly	Glu	Asp	
					1125					1130				1135			
85	ACT	CTA	TTA	GTT	ATG	TTC	TAT	TCG	ATG	CAG	AGT	AGT	TAT	AGC	TCC	TAT	3456
	Thr	Leu	Leu	Val	Met	Phe	Tyr	Ser	Met	Gln	Ser	Ser	Tyr	Ser	Ser	Tyr	
				1140					1145				1150				
90	ACC	GAT	AAT	AAT	GCG	CCG	GTC	ACT	GGG	CTA	TAT	ATT	TTC	GCT	GAT	ATG	3504

	Thr	Asp	Asn	Asn	Ala	Pro	Val	Thr	Gly	Leu	Tyr	Ile	Phe	Ala	Asp	Met	
	1155							1160					1165				
5	TCA	TCA	GAC	AAT	ATG	ACG	AAT	GCA	CAA	GCA	ACT	AAC	TAT	TGG	AAT	AAC	3552
	Ser	Ser	Asp	Asn	Met	Thr	Asn	Ala	Gln	Ala	Thr	Asn	Tyr	Trp	Asn	Asn	
	1170						1175					1180					
10	AGT	TAT	CCG	CAA	TTT	GAT	ACT	GTG	ATG	GCA	GAT	CCG	GAT	AGC	GAC	AAT	3600
	Ser	Tyr	Pro	Gln	Phe	Asp	Thr	Val	Met	Ala	Asp	Pro	Asp	Ser	Asp	Asn	
	1185					1190					1195					1200	
15	AAA	AAA	GTC	ATA	ACC	AGA	AGA	GTT	AAT	AAC	CGT	TAT	CCG	GAG	GAT	TAT	3648
	Lys	Lys	Val	Ile	Thr	Arg	Arg	Val	Asn	Asn	Arg	Tyr	Ala	Glu	Asp	Tyr	
					1205					1210					1215		
	GAA	ATT	CCT	TCC	TCT	GTG	ACA	AGT	AAC	AGT	AAT	TAT	TCT	TGG	GGT	GAT	3696
	Glu	Ile	Pro	Ser	Ser	Val	Thr	Ser	Asn	Ser	Asn	Tyr	Ser	Trp	Gly	Asp	
					1220				1225						1230		
20	CAC	AGT	TTA	ACC	ATG	CTT	TAT	GGT	GGT	AGT	GTT	CCT	AAT	ATT	ACT	TTT	3744
	His	Ser	Leu	Thr	Met	Leu	Tyr	Gly	Gly	Ser	Val	Pro	Asn	Ile	Thr	Phe	
					1235				1240					1245			
25	GAA	TCG	GCG	GCA	GAA	GAT	TTA	AGG	CTA	TCT	ACC	AAT	ATG	GCA	TTG	AGT	3792
	Glu	Ser	Ala	Ala	Glu	Asp	Leu	Arg	Leu	Ser	Thr	Asn	Met	Ala	Leu	Ser	
		1250					1255					1260					
30	ATT	ATT	CAT	AAT	GGA	TAT	GCG	GGA	ACC	CGC	CGT	ATA	CAA	TGT	AAT	CTT	3840
	Ile	Ile	His	Asn	Gly	Tyr	Ala	Gly	Thr	Arg	Arg	Ile	Gln	Cys	Asn	Leu	
	1265					1270					1275					1280	
	ATG	AAA	CAA	TAC	GCT	TCA	TTA	GGT	GAT	AAA	TTT	ATA	ATT	TAT	GAT	TCA	3888
	Met	Lys	Gln	Tyr	Ala	Ser	Leu	Gly	Asp	Lys	Phe	Ile	Ile	Tyr	Asp	Ser	
					1285					1290					1295		
35	TCA	TTT	GAT	GAT	GCA	AAC	CGT	TTT	AAT	CTG	GTG	CCA	TTG	TTT	AAA	TTC	3936
	Ser	Phe	Asp	Asp	Ala	Asn	Arg	Phe	Asn	Leu	Val	Pro	Leu	Phe	Lys	Phe	
					1300				1305						1310		
40	GGA	AAA	GAC	GAG	AAC	TCA	GAT	GAT	AGT	ATT	TGT	ATA	TAT	AAT	GAA	AAC	3984
	Gly	Lys	Asp	Glu	Asn	Ser	Asp	Asp	Ser	Ile	Cys	Ile	Tyr	Asn	Glu	Asn	
					1315				1320					1325			
45	CCT	TCC	TCT	GAA	GAT	AAG	AAG	TGG	TAT	TTT	TCT	TCG	AAA	GAT	GAC	AAT	4032
	Pro	Ser	Ser	Glu	Asp	Lys	Lys	Trp	Tyr	Phe	Ser	Ser	Lys	Asp	Asp	Asn	
		1330					1335					1340					
50	AAA	ACA	GCG	GAT	TAT	AAT	GGT	GGA	ACT	CAA	TGT	ATA	GAT	GCT	GGA	ACC	4080
	Lys	Thr	Ala	Asp	Tyr	Asn	Gly	Gly	Thr	Gln	Cys	Ile	Asp	Ala	Gly	Thr	
	1345					1350					1355					1360	
	AGT	AAC	AAA	GAT	TTT	TAT	TAT	AAT	CTC	CAG	GAG	ATT	GAA	GTA	ATT	AGT	4128
	Ser	Asn	Lys	Asp	Phe	Tyr	Tyr	Asn	Leu	Gln	Glu	Ile	Glu	Val	Ile	Ser	
					1365					1370					1375		
55	GTT	ACT	GGT	GGG	TAT	TGG	TCG	AGT	TAT	AAA	ATA	TCC	AAC	CCG	ATT	AAT	4176
	Val	Thr	Gly	Gly	Tyr	Trp	Ser	Ser	Tyr	Lys	Ile	Ser	Asn	Pro	Ile	Asn	
					1380				1385					1390			
60	ATC	AAT	ACG	GGC	ATT	GAT	AGT	GCT	AAA	GTA	AAA	GTC	ACC	GTA	AAA	GCG	4224
	Ile	Asn	Thr	Gly	Ile	Asp	Ser	Ala	Lys	Val	Lys	Val	Thr	Val	Lys	Ala	
					1395				1400					1405			
65	GGT	GGT	GAC	GAT	CAA	ATC	TTT	ACT	GCT	GAT	AAT	AGT	ACC	TAT	GTT	CCT	4272
	Gly	Gly	Asp	Asp	Gln	Ile	Phe	Thr	Ala	Asp	Asn	Ser	Thr	Tyr	Val	Pro	
		1410					1415					1420					
70	CAG	CAA	CCG	GCA	CCC	AGT	TTT	GAG	GAG	ATG	ATT	TAT	CAG	TTC	AAT	AAC	4320
	Gln	Gln	Pro	Ala	Pro	Ser	Phe	Glu	Glu	Met	Ile	Tyr	Gln	Phe	Asn	Asn	
	1425					1430					1435					1440	

CTG ACA ATA GAT TGT AAG AAT TTA AAT TTC ATC GAC AAT CAG GCA CAT 4163
 Leu Thr Ile Asp Cys Lys Asn Leu Asn Phe Ile Asp Asn Gln Ala His
 1445 1450 1455

5 ATT GAG ATT GAT TTC ACC GCT ACG GCA CAA GAT GGC CGA TTC TTG CGT 4416
 Ile Glu Ile Asp Phe Thr Ala Thr Ala Gln Asp Gly Arg Phe Leu Gly
 1460 1465 1470

10 GCA GAA ACT TTT ATT ATC CCG GTA ACT AAA AAA GTT CTC GGT ACT GAG 4464
 Ala Glu Thr Phe Ile Ile Pro Val Thr Lys Lys Val Leu Gly Thr Glu
 1475 1480 1485

15 AAC GTG ATT GCG TTA TAT AGC GAA AAT AAC GGT GTT CAA TAT ATG CAA 4512
 Asn Val Ile Ala Leu Tyr Ser Glu Asn Asn Gly Val Gln Tyr Met Gln
 1490 1495 1500

20 ATT GGC GCA TAT CGT ACC CGT TTG AAT ACG TTA TTC GCT CAA CAG TTG 4560
 Ile Gly Ala Tyr Arg Thr Arg Leu Asn Thr Leu Phe Ala Gln Gln Leu
 1505 1510 1515 1520

GTT AGC CGT GCT AAT CGT GGC ATT GAT GCA GTG CTC AGT ATG GAA ACT 4608
 Val Ser Arg Ala Asn Arg Gly Ile Asp Ala Val Leu Ser Met Glu Thr
 1525 1530 1535

25 CAG AAT ATT CAG GAA CCG CAA TTA GGA GCG GGC ACA TAT GTG CAG CTT 4656
 Gln Asn Ile Gln Glu Pro Gln Leu Gly Ala Gly Thr Tyr Val Gln Leu
 1540 1545 1550

30 GTG TTG GAT AAA TAT GAT GAG TCT ATT CAT GGC ACT AAT AAA AGC TTT 4704
 Val Leu Asp Lys Tyr Asp Glu Ser Ile His Gly Thr Asn Lys Ser Phe
 1555 1560 1565

35 GCT ATT GAA TAT GTT GAT ATA TTT AAA GAG AAC GAT AGT TTT GTG ATT 4752
 Ala Ile Glu Tyr Val Asp Ile Phe Lys Glu Asn Asp Ser Phe Val Ile
 1570 1575 1580

40 TAT CAA GGA GAA CTT AGC GAA ACA AGT CAA ACT GTT GTG AAA GTT TTC 4800
 Tyr Gln Gly Glu Leu Ser Glu Thr Ser Gln Thr Val Val Lys Val Phe
 1585 1590 1595 1600

TTA TCC TAT TTT ATA GAG GCG ACT GGA AAT AAG AAC CAC TTA TGG GTA 4848
 Leu Ser Tyr Phe Ile Glu Ala Thr Gly Asn Lys Asn His Leu Trp Val
 1605 1610 1615

45 CGT GCT AAA TAC CAA AAG GAA ACG ACT GAT AAG ATC TTG TTC GAC CGT 4896
 Arg Ala Lys Tyr Gln Lys Glu Thr Thr Asp Lys Ile Leu Phe Asp Arg
 1620 1625 1630

50 ACT GAT GAG AAA GAT CCG CAC GGT TGG TTT CTC AGC GAC GAT CAC AAG 4944
 Thr Asp Glu Lys Asp Pro His Gly Trp Phe Leu Ser Asp Asp His Lys
 1635 1640 1645

55 ACC TTT AGT GGT CTC TCT TCC GCA CAG GCA TTA AAG AAC GAC AGT GAA 4992
 Thr Phe Ser Gly Leu Ser Ser Ala Gln Ala Leu Lys Asn Asp Ser Glu
 1650 1655 1660

60 CCG ATG GAT TTC TCT GGC GCC AAT GCT CTC TAT TTC TGG GAA CTG TTC 5040
 Pro Met Asp Phe Ser Gly Ala Asn Ala Leu Tyr Phe Trp Glu Leu Phe
 1665 1670 1675 1680

TAT TAC ACG CCG ATG ATG ATG GCT CAT CGT TTG TTG CAG GAA CAG AAT 5088
 Tyr Tyr Thr Pro Met Met Met Ala His Arg Leu Leu Gln Glu Gln Asn
 1685 1690 1695

65 TTT GAT GCG GCG AAC CAT TGG TTC CGT TAT GTC TGG AGT CCA TCC GGT 5136
 Phe Asp Ala Ala Asn His Trp Phe Arg Tyr Val Trp Ser Pro Ser Gly
 1700 1705 1710

70 TAT ATC GTT GAT GGT AAA ATT GCT ATC TAC CAC TGG AAC GTG CGA CCG 5184
 Tyr Ile Val Asp Gly Lys Ile Ala Ile Tyr His Trp Asn Val Arg Pro
 1715 1720 1725

CTG GAA GAA GAC ACC AGT TGG AAT GCA CAA CAA CTG GAC TCC ACC GAT 5231
 Leu Glu Glu Asp Thr Ser Trp Asn Ala Gln Gln Leu Asp Ser Thr Asp
 1730 1735 1740

5 CCA GAT GCT GTA GCC CAA GAT GAT CCG ATG CAC TAC AAG GTG GCT ACC 5280
 Pro Asp Ala Val Ala Gln Asp Asp Pro Met His Tyr Lys Val Ala Thr
 1745 1750 1755 1760

10 TTT ATG GCG ACG TTG GAT CTG CTA ATG GCC CGT CGT GAT GCT GCT TAC 5328
 Phe Met Ala Thr Leu Asp Leu Leu Met Ala Arg Gly Asp Ala Ala Tyr
 1765 1770 1775

15 CCC CAG TTA GAG CGT GAT ACG TTG GCT GAA GCT AAA ATG TGG TAT ACA 5376
 Arg Gln Leu Glu Arg Asp Thr Leu Ala Glu Ala Lys Met Trp Tyr Thr
 1780 1785 1790

20 CAG GCG CTT AAT CTG TTG GGT GAT GAG CCA CAA GTG ATG CTG AGT ACG 5424
 Gln Ala Leu Asn Leu Leu Gly Asp Glu Pro Gln Val Met Leu Ser Thr
 1795 1800 1805

ACT TGG GCT AAT CCA ACA TTG GGT AAT GCT GCT TCA AAA ACC ACA CAG 5472
 Thr Trp Ala Asn Pro Thr Leu Gly Asn Ala Ala Ser Lys Thr Thr Gln
 1810 1815 1820

25 CAG GTT CGT CAG CAA GTG CTT ACC CAG TTG CGT CTC AAT AGC AGG GTA 5520
 Gln Val Arg Gln Gln Val Leu Thr Gln Leu Arg Leu Asn Ser Arg Val
 1825 1830 1835 1840

30 AAA ACC CCG TTG 5532
 Lys Thr Pro Leu
 1844

35 (2) INFORMATION FOR SEQ ID NO:53:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1844 amino acids
 (B) TYPE: amino acids
 (C) STRANDEDNESS: single
 40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53 (TcbAii):

Features	From	To	Description
Peptide	1	1844	TcbAii peptide
Fragment	1	11	(SEQ ID NO:1)
Fragment	978	990	(SEQ ID NO:23)
Fragment	1387	1401	(SEQ ID NO:22)
Fragment	1484	1505	(SEQ ID NO:24)
Fragment	1527	1552	(SEQ ID NO:21)

55 Phe Ile Gln Gly Tyr Ser Asp Leu Phe Gly Asn Arg Ala Asp Asn Tyr
 1 5 10 15

Ala Ala Pro Gly Ser Val Ala Ser Met Phe Ser Pro Ala Ala Tyr Leu
 20 25 30

60 Thr Glu Leu Tyr Arg Glu Ala Lys Asn Leu His Asp Ser Ser Ser Ile
 35 40 45

Tyr Tyr Leu Asp Lys Arg Arg Pro Asp Leu Ala Ser Leu Met Leu Ser
 50 55 60

65 Gln Lys Asn Met Asp Glu Glu Ile Ser Thr Leu Ala Leu Ser Asn Glu
 65 70 75 80

Leu Cys Leu Ala Gly Ile Glu Thr Lys Thr Gly Lys Ser Gln Asp Glu

	85	90	95
5	Val Met Asp Met Leu Ser Thr Tyr Arg Leu Ser Gly Glu Thr Pro Tyr 100 105 110		
	His His Ala Tyr Glu Thr Val Arg Glu Ile Val His Glu Arg Asp Pro 115 120 125		
10	Gly Phe Arg His Leu Ser Gln Ala Pro Ile Val Ala Ala Lys Leu Asp 130 135 140		
	Pro Val Thr Leu Leu Gly Ile Ser Ser His Ile Ser Pro Glu Leu Tyr 145 150 155 160		
15	Asn Leu Leu Ile Glu Glu Ile Pro Glu Lys Asp Glu Ala Ala Leu Asp 165 170 175		
	Thr Leu Tyr Lys Thr Asn Phe Gly Asp Ile Thr Thr Ala Gln Leu Met 180 185 190		
20	Ser Pro Ser Tyr Leu Ala Arg Tyr Tyr Gly Val Ser Pro Glu Asp Ile 195 200 205		
	Ala Tyr Val Thr Thr Ser Leu Ser His Val Gly Tyr Ser Ser Asp Ile 210 215 220		
	Leu Val Ile Pro Leu Val Asp Gly Val Gly Lys Met Glu Val Val Arg 225 230 235 240		
30	Val Thr Arg Thr Pro Ser Asp Asn Tyr Thr Ser Gln Thr Asn Tyr Ile 245 250 255		
	Glu Leu Tyr Pro Gln Gly Gly Asp Asn Tyr Leu Ile Lys Tyr Asn Leu 260 265 270		
35	Ser Asn Ser Phe Gly Leu Asp Asp Phe Tyr Leu Gln Tyr Lys Asp Gly 275 280 285		
	Ser Ala Asp Trp Thr Glu Ile Ala His Asn Pro Tyr Pro Asp Met Val 290 295 300		
	Ile Asn Gln Lys Tyr Glu Ser Gln Ala Thr Ile Lys Arg Ser Asp Ser 305 310 315 320		
45	Asp Asn Ile Leu Ser Ile Gly Leu Gln Arg Trp His Ser Gly Ser Tyr 325 330 335		
	Asn Phe Ala Ala Ala Asn Phe Lys Ile Asp Gln Tyr Ser Pro Lys Ala 340 345 350		
50	Phe Leu Leu Lys Met Asn Lys Ala Ile Arg Leu Leu Lys Ala Thr Gly 355 360 365		
	Leu Ser Phe Ala Thr Leu Glu Arg Ile Val Asp Ser Val Asn Ser Thr 370 375 380		
	Lys Ser Ile Thr Val Glu Val Leu Asn Lys Val Tyr Arg Val Lys Phe 385 390 395 400		
60	Tyr Ile Asp Arg Tyr Gly Ile Ser Glu Glu Thr Ala Ala Ile Leu Ala 405 410 415		
	Asn Ile Asn Ile Ser Gln Gln Ala Val Gly Asn Gln Leu Ser Gln Phe 420 425 430		
65	Glu Gln Leu Phe Asn His Pro Pro Leu Asn Gly Ile Arg Tyr Glu Ile 435 440 445		
	Ser Glu Asp Asn Ser Lys His Leu Pro Asn Pro Asp Leu Asn Leu Lys 450 455 460		

Pro Asp Ser Thr Gly Asp Asp Gln Arg Lys Ala Val Leu Lys Arg Ala
 465 470 475 480
 5 Phe Gln Val Asn Ala Ser Glu Leu Tyr Gln Met Leu Leu Ile Thr Asp
 485 490 495
 Arg Lys Glu Asp Gly Val Ile Lys Asn Asn Leu Glu Asn Leu Ser Asp
 500 505 510
 10 Leu Tyr Leu Val Ser Leu Leu Ala Gln Ile His Asn Leu Thr Ile Ala
 515 520 525
 Glu Leu Asn Ile Leu Leu Val Ile Cys Gly Tyr Gly Asp Thr Asn Ile
 530 535 540
 15 Tyr Gln Ile Thr Asp Asp Asn Leu Ala Lys Ile Val Glu Thr Leu Leu
 545 550 555 560
 20 Trp Ile Thr Gln Trp Leu Lys Thr Gln Lys Trp Thr Val Thr Asp Leu
 565 570 575
 Phe Leu Met Thr Thr Ala Thr Tyr Ser Thr Thr Leu Thr Pro Glu Ile
 580 585 590
 25 Ser Asn Leu Thr Ala Thr Leu Ser Ser Thr Leu His Gly Lys Glu Ser
 595 600 605
 Leu Ile Gly Glu Asp Leu Lys Arg Ala Met Ala Pro Cys Phe Thr Ser
 610 615 620
 30 Ala Leu His Leu Thr Ser Gln Glu Val Ala Tyr Asp Leu Leu Leu Trp
 625 630 635 640
 35 Ile Asp Gln Ile Gln Pro Ala Gln Ile Thr Val Asp Gly Phe Trp Glu
 645 650 655
 Glu Val Gln Thr Thr Pro Thr Ser Leu Lys Val Ile Thr Phe Ala Gln
 660 665 670
 40 Val Leu Ala Gln Leu Ser Leu Ile Tyr Arg Arg Ile Gly Leu Ser Glu
 675 680 685
 Thr Glu Leu Ser Leu Ile Val Thr Gln Ser Ser Leu Leu Val Ala Gly
 690 695 700
 45 Lys Ser Ile Leu Asp His Gly Leu Leu Thr Leu Met Ala Leu Glu Gly
 705 710 715 720
 50 Phe His Thr Trp Val Asn Gly Leu Gly Gln His Ala Ser Leu Ile Leu
 725 730 735
 Ala Ala Leu Lys Asp Gly Ala Leu Thr Val Thr Asp Val Ala Gln Ala
 740 745 750
 55 Met Asn Lys Glu Glu Ser Leu Leu Gln Met Ala Ala Asn Gln Val Glu
 755 760 765
 Lys Asp Leu Thr Lys Leu Thr Ser Trp Thr Gln Ile Asp Ala Ile Leu
 770 775 780
 60 Gln Trp Leu Gln Met Ser Ser Ala Leu Ala Val Ser Pro Leu Asp Leu
 785 790 795 800
 65 Ala Gly Met Met Ala Leu Lys Tyr Gly Ile Asp His Asn Tyr Ala Ala
 805 810 815
 Trp Gln Ala Ala Ala Ala Leu Met Ala Asp His Ala Asn Gln Ala
 820 825 830
 70 Gln Lys Lys Leu Asp Glu Thr Phe Ser Lys Ala Leu Cys Asn Tyr Tyr
 835 840 845

	Ile	Asn	Ala	Val	Val	Asp	Ser	Ala	Ala	Gly	Val	Arg	Asp	Arg	Asn	Gly	
		350					855					860					
5	Leu	Tyr	Thr	Tyr	Leu	Leu	Ile	Asp	Asn	Gln	Val	Ser	Ala	Asp	Val	Ile	
	865				870					875						880	
	Thr	Ser	Arg	Ile	Ala	Glu	Ala	Ile	Ala	Gly	Ile	Gln	Leu	Tyr	Val	Asn	
				885						890					895		
10	Arg	Ala	Leu	Asn	Arg	Asp	Glu	Gly	Gln	Leu	Ala	Ser	Asp	Val	Ser	Thr	
				900					905					910			
	Arg	Gln	Phe	Phe	Thr	Asp	Trp	Glu	Arg	Tyr	Asn	Lys	Arg	Tyr	Ser	Thr	
15			915					920					925				
	Trp	Ala	Gly	Val	Ser	Glu	Leu	Val	Tyr	Tyr	Pro	Glu	Asn	Tyr	Val	Asp	
	930						935					940					
20	Pro	Thr	Gln	Arg	Ile	Gly	Gln	Thr	Lys	Met	Met	Asp	Ala	Leu	Leu	Gln	
	945					950					955					960	
	Ser	Ile	Asn	Gln	Ser	Gln	Leu	Asn	Ala	Asp	Thr	Val	Glu	Asp	Ala	Phe	
					965					970					975		
25	Lys	Thr	Tyr	Leu	Thr	Ser	Phe	Glu	Gln	Val	Ala	Asn	Leu	Lys	Val	Ile	
			980						985					990			
	Ser	Ala	Tyr	His	Asp	Asn	Val	Asn	Val	Asp	Gln	Gly	Leu	Thr	Tyr	Phe	
30			995					1000					1005				
	Ile	Gly	Ile	Asp	Gln	Ala	Ala	Pro	Gly	Thr	Tyr	Tyr	Trp	Arg	Ser	Val	
		1010					1015					1020					
35	Asp	His	Ser	Lys	Cys	Glu	Asn	Gly	Lys	Phe	Ala	Ala	Asn	Ala	Trp	Gly	
	1025					1030					1035					1040	
	Glu	Trp	Asn	Lys	Ile	Thr	Cys	Ala	Val	Asn	Pro	Trp	Lys	Asn	Ile	Ile	
					1045					1050					1055		
40	Arg	Pro	Val	Val	Tyr	Met	Ser	Arg	Leu	Tyr	Leu	Leu	Trp	Leu	Glu	Gln	
				1060					1065					1070			
	Gln	Ser	Lys	Lys	Ser	Asp	Asp	Gly	Lys	Thr	Thr	Ile	Tyr	Gln	Tyr	Asn	
45			1075					1080					1085				
	Leu	Lys	Leu	Ala	His	Ile	Arg	Tyr	Asp	Gly	Ser	Trp	Asn	Thr	Pro	Phe	
		1090					1095					1100					
50	Thr	Phe	Asp	Val	Thr	Glu	Lys	Val	Lys	Asn	Tyr	Thr	Ser	Ser	Thr	Asp	
	1105					1110					1115					1120	
	Ala	Ala	Glu	Ser	Leu	Gly	Leu	Tyr	Cys	Thr	Gly	Tyr	Gln	Gly	Glu	Asp	
					1125					1130					1135		
55	Thr	Leu	Leu	Val	Met	Phe	Tyr	Ser	Met	Gln	Ser	Ser	Tyr	Ser	Ser	Tyr	
				1140					1145					1150			
	Thr	Asp	Asn	Asn	Ala	Pro	Val	Thr	Gly	Leu	Tyr	Ile	Phe	Ala	Asp	Met	
60			1155					1160					1165				
	Ser	Ser	Asp	Asn	Met	Thr	Asn	Ala	Gln	Ala	Thr	Asn	Tyr	Trp	Asn	Asn	
		1170					1175					1180					
65	Ser	Tyr	Pro	Gln	Phe	Asp	Thr	Val	Met	Ala	Asp	Pro	Asp	Ser	Asp	Asn	
	1185					1190					1195					1200	
	Lys	Lys	Val	Ile	Thr	Arg	Arg	Val	Asn	Asn	Arg	Tyr	Ala	Glu	Asp	Tyr	
				1205						1210					1215		
70	Glu	Ile	Pro	Ser	Ser	Val	Thr	Ser	Asn	Ser	Asn	Tyr	Ser	Trp	Gly	Asp	

	1220	1225	1230
	His Ser Leu Thr Met Leu Tyr Gly Gly Ser Val Pro Asn Ile Thr Phe 1235 1240 1245		
5	Glu Ser Ala Ala Glu Asp Leu Arg Leu Ser Thr Asn Met Ala Leu Ser 1250 1255 1260		
10	Ile Ile His Asn Gly Tyr Ala Gly Thr Arg Arg Ile Gln Cys Asn Leu 1265 1270 1275 1280		
	Met Lys Gln Tyr Ala Ser Leu Gly Asp Lys Phe Ile Ile Tyr Asp Ser 1285 1290 1295		
15	Ser Phe Asp Asp Ala Asn Arg Phe Asn Leu Val Pro Leu Phe Lys Phe 1300 1305 1310		
	Gly Lys Asp Glu Asn Ser Asp Asp Ser Ile Cys Ile Tyr Asn Glu Asn 1315 1320 1325		
20	Pro Ser Ser Glu Asp Lys Lys Trp Tyr Phe Ser Ser Lys Asp Asp Asn 1330 1335 1340		
25	Lys Thr Ala Asp Tyr Asn Gly Gly Thr Gln Cys Ile Asp Ala Gly Thr 1345 1350 1355 1360		
	Ser Asn Lys Asp Phe Tyr Tyr Asn Leu Gln Glu Ile Glu Val Ile Ser 1365 1370 1375		
30	Val Thr Gly Gly Tyr Trp Ser Ser Tyr Lys Ile Ser Asn Pro Ile Asn 1380 1385 1390		
	Ile Asn Thr Gly Ile Asp Ser Ala Lys Val Lys Val Thr Val Lys Ala 1395 1400 1405		
35	Gly Gly Asp Asp Gln Ile Phe Thr Ala Asp Asn Ser Thr Tyr Val Pro 1410 1415 1420		
40	Gln Gln Pro Ala Pro Ser Phe Glu Glu Met Ile Tyr Gln Phe Asn Asn 1425 1430 1435 1440		
	Leu Thr Ile Asp Cys Lys Asn Leu Asn Phe Ile Asp Asn Gln Ala His 1445 1450 1455		
45	Ile Glu Ile Asp Phe Thr Ala Thr Ala Gln Asp Gly Arg Phe Leu Gly 1460 1465 1470		
	Ala Glu Thr Phe Ile Ile Pro Val Thr Lys Lys Val Leu Gly Thr Glu 1475 1480 1485		
50	Asn Val Ile Ala Leu Tyr Ser Glu Asn Asn Gly Val Gln Tyr Met Gln 1490 1495 1500		
55	Ile Gly Ala Tyr Arg Thr Arg Leu Asn Thr Leu Phe Ala Gln Gln Leu 1505 1510 1515 1520		
	Val Ser Arg Ala Asn Arg Gly Ile Asp Ala Val Leu Ser Met Glu Thr 1525 1530 1535		
60	Gln Asn Ile Gln Glu Pro Gln Leu Gly Ala Gly Thr Tyr Val Gln Leu 1540 1545 1550		
	Val Leu Asp Lys Tyr Asp Glu Ser Ile His Gly Thr Asn Lys Ser Phe 1555 1560 1565		
65	Ala Ile Glu Tyr Val Asp Ile Phe Lys Glu Asn Asp Ser Phe Val Ile 1570 1575 1580		
70	Tyr Gln Gly Glu Leu Ser Glu Thr Ser Gln Thr Val Val Lys Val Phe 1585 1590 1595 1600		

Leu Ser Tyr Phe Ile Glu Ala Thr Gly Asn Lys Asn His Leu Trp Val
 1605 1610 1615
 5 Arg Ala Lys Tyr Gln Lys Glu Thr Thr Asp Lys Ile Leu Phe Asp Arg
 1620 1625 1630
 Thr Asp Glu Lys Asp Pro His Gly Trp Phe Leu Ser Asp Asp His Lys
 1635 1640 1645
 10 Thr Phe Ser Gly Leu Ser Ser Ala Gln Ala Leu Lys Asn Asp Ser Glu
 1650 1655 1660
 Pro Met Asp Phe Ser Gly Ala Asn Ala Leu Tyr Phe Trp Glu Leu Phe
 1665 1670 1675 1680
 15 Tyr Tyr Thr Pro Met Met Met Ala His Arg Leu Leu Gln Glu Gln Asn
 1685 1690 1695
 20 Phe Asp Ala Ala Asn His Trp Phe Arg Tyr Val Trp Ser Pro Ser Gly
 1700 1705 1710
 Tyr Ile Val Asp Gly Lys Ile Ala Ile Tyr His Trp Asn Val Arg Pro
 1715 1720 1725
 25 Leu Glu Glu Asp Thr Ser Trp Asn Ala Gln Gln Leu Asp Ser Thr Asp
 1730 1735 1740
 Pro Asp Ala Val Ala Gln Asp Asp Pro Met His Tyr Lys Val Ala Thr
 1745 1750 1755 1760
 30 Phe Met Ala Thr Leu Asp Leu Leu Met Ala Arg Gly Asp Ala Ala Tyr
 1765 1770 1775
 35 Arg Gln Leu Glu Arg Asp Thr Leu Ala Glu Ala Lys Met Trp Tyr Thr
 1780 1785 1790
 Gln Ala Leu Asn Leu Leu Gly Asp Glu Pro Gln Val Met Leu Ser Thr
 1795 1800 1805
 40 Thr Trp Ala Asn Pro Thr Leu Gly Asn Ala Ala Ser Lys Thr Thr Gln
 1810 1815 1820
 Gln Val Arg Gln Gln Val Leu Thr Gln Leu Arg Leu Asn Ser Arg Val
 1825 1830 1835 1840
 45 Lys Thr Pro Leu
 1844

50 (2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54 (TcbAiii coding region):

CTA GGA ACA GCC AAT TCC CTG ACC GCT TTA TTC CTG CCG CAG GAA AAT 48
 Leu Gly Thr Ala Asn Ser Leu Thr Ala Leu Phe Leu Pro Gln Glu Asn
 1 5 10 15
 65 AGC AAG CTC AAA GGC TAC TCG CCG ACA CTG GCG CAG CGT ATG TTT AAT 96
 Ser Lys Leu Lys Gly Tyr Trp Arg Thr Leu Ala Gln Arg Met Phe Asn
 20 25 30

	TTA	CGT	CAT	AAT	CTG	TCG	ATT	GAC	GGC	CAG	CCG	CTC	TCC	TTG	CCG	CTG	144
	Leu	Arg	His	Asn	Leu	Ser	Ile	Asp	Gly	Gln	Pro	Leu	Ser	Leu	Pro	Leu	
			35					40					45				
5	TAT	GCT	AAA	CCG	GCT	GAT	CCA	AAA	GCT	TTA	CTG	AGT	GCG	GCG	GTT	TCA	132
	Tyr	Ala	Lys	Pro	Ala	Asp	Pro	Lys	Ala	Leu	Leu	Ser	Ala	Ala	Val	Ser	
		50					55					60					
10	GCT	TCT	CAA	GGG	GGA	GCC	GAC	TTG	CCG	AAG	GCG	CCG	CTG	ACT	ATT	CAC	240
	Ala	Ser	Gln	Gly	Gly	Ala	Asp	Leu	Pro	Lys	Ala	Pro	Leu	Thr	Ile	His	
	65					70					75					80	
15	CGC	TTC	CCT	CAA	ATG	CTA	GAA	GGG	GCA	CGG	GCG	TTG	GTT	AAC	CAG	CTT	288
	Arg	Phe	Pro	Gln	Met	Leu	Glu	Gly	Ala	Arg	Gly	Leu	Val	Asn	Gln	Leu	
					85					90					95		
20	ATA	CAG	TTC	GGT	AGT	TCA	CTA	TTG	GGG	TAC	AGT	GAG	CGT	CAG	GAT	CCG	336
	Ile	Gln	Phe	Gly	Ser	Ser	Leu	Leu	Gly	Tyr	Ser	Glu	Arg	Gln	Asp	Ala	
				100					105					110			
25	GAA	GCT	ATG	AGT	CAA	CTA	CTG	CAA	ACC	CAA	GCC	AGC	GAG	TTA	ATA	CTG	384
	Glu	Ala	Met	Ser	Gln	Leu	Leu	Gln	Thr	Gln	Ala	Ser	Glu	Leu	Ile	Leu	
			115					120					125				
30	ACC	AGT	ATT	CGT	ATG	CAG	GAT	AAC	CAA	TTG	GCA	GAG	CTG	GAT	TCG	GAA	432
	Thr	Ser	Ile	Arg	Met	Gln	Asp	Asn	Gln	Leu	Ala	Glu	Leu	Asp	Ser	Glu	
		130					135						140				
35	AAA	ACC	GCC	TTG	CAA	GTC	TCT	TTA	GCT	GGA	GTG	CAA	CAA	CGG	TTT	GAC	480
	Lys	Thr	Ala	Leu	Gln	Val	Ser	Leu	Ala	Gly	Val	Gln	Gln	Arg	Phe	Asp	
	145					150					155					160	
40	AGC	TAT	AGC	CAA	CTG	TAT	GAG	GAG	AAC	ATC	AAC	GCA	GGT	GAG	CAG	CGA	528
	Ser	Tyr	Ser	Gln	Leu	Tyr	Glu	Glu	Asn	Ile	Asn	Ala	Gly	Glu	Gln	Arg	
					165					170					175		
45	GCG	CTG	GCG	TTA	CGC	TCA	GAA	TCT	GCT	ATT	GAG	TCT	CAG	GGA	GCG	CAG	576
	Ala	Leu	Ala	Leu	Arg	Ser	Glu	Ser	Ala	Ile	Glu	Ser	Gln	Gly	Ala	Gln	
				180					185					190			
50	ATT	TCC	CGT	ATG	GCA	GGC	GCG	GGT	GTT	GAT	ATG	GCA	CCA	AAT	ATC	TTC	624
	Ile	Ser	Arg	Met	Ala	Gly	Ala	Gly	Val	Asp	Met	Ala	Pro	Asn	Ile	Phe	
			195					200					205				
55	GGC	CTG	GCT	GAT	GGC	GGC	ATG	CAT	TAT	GGT	GCT	ATT	GCC	TAT	GCC	ATC	672
	Gly	Leu	Ala	Asp	Gly	Gly	Met	His	Tyr	Gly	Ala	Ile	Ala	Tyr	Ala	Ile	
		210					215					220					
60	GCT	GAC	GGT	ATT	GAG	TTG	AGT	GCT	TCT	GCC	AAG	ATG	GTT	GAT	GCG	GAG	720
	Ala	Asp	Gly	Ile	Glu	Leu	Ser	Ala	Ser	Ala	Lys	Met	Val	Asp	Ala	Glu	
	225					230					235					240	
65	AAA	GTT	GCT	CAG	TCG	GAA	ATA	TAT	CGC	CGT	CGC	CGT	CAA	GAA	TGG	AAA	768
	Lys	Val	Ala	Gln	Ser	Glu	Ile	Tyr	Arg	Arg	Arg	Arg	Gln	Glu	Trp	Lys	
					245					250					255		
70	ATT	CAG	CGT	GAC	AAC	GCA	CAA	GCG	GAG	ATT	AAC	CAG	TTA	AAC	GCG	CAA	816
	Ile	Gln	Arg	Asp	Asn	Ala	Gln	Ala	Glu	Ile	Asn	Gln	Leu	Asn	Ala	Gln	
				260					265					270			
75	CTG	GAA	TCA	CTG	TCT	ATT	CGC	CGT	GAA	GCC	GCT	GAA	ATG	CAA	AAA	GAG	864
	Leu	Glu	Ser	Leu	Ser	Ile	Arg	Arg	Glu	Ala	Ala	Glu	Met	Gln	Lys	Glu	
			275					280					285				
80	TAC	CTG	AAA	ACC	CAG	CAA	GCT	CAG	GCG	CAG	GCA	CAA	CTT	ACT	TTC	TTA	912
	Tyr	Leu	Lys	Thr	Gln	Gln	Ala	Gln	Ala	Gln	Ala	Gln	Leu	Thr	Phe	Leu	
		290					295					300					
85	AGA	AGC	AAA	TTC	AGT	AAT	CAA	GCG	TTA	TAT	AGT	TGG	TTA	CGA	GCG	CGT	960
	Arg	Ser	Lys	Phe	Ser	Asn	Gln	Ala	Leu	Tyr	Ser	Trp	Leu	Arg	Gly	Arg	
	305					310					315					320	

5	TTG TCA GGT ATT TAT TTC CAG TTC TAT GAC TTG GCC GTA TCA CGT TSC 1008 Leu Ser Gly Ile Tyr Phe Gln Phe Tyr Asp Leu Ala Val Ser Arg Cys 335
10	CTG ATG GCA GAG CAA TCC TAT CAA TGG GAA GCT AAT GAT AAT TCC ATT 1056 Leu Met Ala Glu Gln Ser Tyr Gln Trp Glu Ala Asn Asp Asn Ser Ile 350
15	AGC TTT GTC AAA CCG GGT GCA TGG CAA GGA ACT TAC GCC GGC TTA TTG 1104 Ser Phe Val Lys Pro Gly Ala Trp Gln Gly Thr Tyr Ala Gly Leu Leu 365
20	TGT GGA GAA GCT TTG ATA CAA AAT CTG GCA CAA ATG GAA GAG GCA TAT 1152 Cys Gly Glu Ala Leu Ile Gln Asn Leu Ala Gln Met Glu Glu Ala Tyr 380
25	CTG AAA TGG GAA TCT CGC GCT TTG GAA GTA GAA CGC ACG GTT TCA TTG 1200 Leu Lys Trp Glu Ser Arg Ala Leu Glu Val Glu Arg Thr Val Ser Leu 400
30	GCA GTG GTT TAT GAT TCA CTG GAA GGT AAT GAT CGT TTT AAT TTA GCG 1248 Ala Val Val Tyr Asp Ser Leu Glu Gly Asn Asp Arg Phe Asn Leu Ala 415
35	GAA CAA ATA CCT GCA TTA TTG GAT AAG GGG GAG GGA ACA GCA GGA ACT 1296 Glu Gln Ile Pro Ala Leu Leu Asp Lys Gly Glu Gly Thr Ala Gly Thr 430
40	AAA GAA AAT GGG TTA TCA TTG GCT AAT GCT ATC CTG TCA GCT TCG GTC 1344 Lys Glu Asn Gly Leu Ser Leu Ala Asn Ala Ile Leu Ser Ala Ser Val 445
45	AAA TTG TCC GAC TTG AAA CTG GGA ACG GAT TAT CCA GAC AGT ATC GTT 1392 Lys Leu Ser Asp Leu Lys Leu Gly Thr Asp Tyr Pro Asp Ser Ile Val 460
50	GGT AGC AAC AAG GTT CGT CGT ATT AAG CAA ATC AGT GTT TCG CTA CCT 1440 Gly Ser Asn Lys Val Arg Arg Ile Lys Gln Ile Ser Val Ser Leu Pro 480
55	GCA TTG GTT GGG CCT TAT CAG GAT GTT CAG GCT ATG CTC AGC TAT GGT 1488 Ala Leu Val Gly Pro Tyr Gln Asp Val Gln Ala Met Leu Ser Tyr Gly 495
60	GGC AGT ACT CAA TTG CCG AAA GGT TGT TCA GCG TTG GCT GTG TCT CAT 1536 Gly Ser Thr Gln Leu Pro Lys Gly Cys Ser Ala Leu Ala Val Ser His 510
65	GGT ACC AAT GAT AGT GGT CAG TTC CAG TTG GAT TTC AAT GAC GGC AAA 1584 Gly Thr Asn Asp Ser Gly Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys 525
70	TAC CTG CCA TTT GAA GGT ATT GCT CTT GAT GAT CAG GGT ACA CTG AAT 1632 Tyr Leu Pro Phe Glu Gly Ile Ala Leu Asp Asp Gln Gly Thr Leu Asn 540
75	CTT CAA TTT CCG AAT GCT ACC GAC AAG CAG AAA GCA ATA TTG CAA ACT 1680 Leu Gln Phe Pro Asn Ala Thr Asp Lys Gln Lys Ala Ile Leu Gln Thr 560
80	ATG AGC GAT ATT ATT TTG CAT ATT CGT TAT ACC ATC CGT TAA 1722 Met Ser Asp Ile Ile Leu His Ile Arg Tyr Thr Ile Arg ... 573

70 (2) INFORMATION FOR SEQ ID NO:55:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 amino acids
(B) TYPE: amino acids

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55 (TcbA_{iii}):

10	Leu	Gly	Thr	Ala	Asn	Ser	Leu	Thr	Ala	Leu	Phe	Leu	Pro	Gln	Glu	Asn	
	1				5					10					15		
	Ser	Lys	Leu	Lys	Gly	Tyr	Trp	Arg	Thr	Leu	Ala	Gln	Arg	Met	Phe	Asn	
			20					25						30			
15	Leu	Arg	His	Asn	Leu	Ser	Ile	Asp	Gly	Gln	Pro	Leu	Ser	Leu	Pro	Leu	
			35					40					45				
	Tyr	Ala	Lys	Pro	Ala	Asp	Pro	Lys	Ala	Leu	Leu	Ser	Ala	Ala	Val	Ser	
		50					55					60					
20	Ala	Ser	Gln	Gly	Gly	Ala	Asp	Leu	Pro	Lys	Ala	Pro	Leu	Thr	Ile	His	
	65					70					75					80	
	Arg	Phe	Pro	Gln	Met	Leu	Glu	Gly	Ala	Arg	Gly	Leu	Val	Asn	Gln	Leu	
25					85					90					95		
	Ile	Gln	Phe	Gly	Ser	Ser	Leu	Leu	Gly	Tyr	Ser	Glu	Arg	Gln	Asp	Ala	
			100						105					110			
30	Glu	Ala	Met	Ser	Gln	Leu	Leu	Gln	Thr	Gln	Ala	Ser	Glu	Leu	Ile	Leu	
			115					120					125				
	Thr	Ser	Ile	Arg	Met	Gln	Asp	Asn	Gln	Leu	Ala	Glu	Leu	Asp	Ser	Glu	
		130					135					140					
35	Lys	Thr	Ala	Leu	Gln	Val	Ser	Leu	Ala	Gly	Val	Gln	Gln	Arg	Phe	Asp	
	145					150					155					160	
	Ser	Tyr	Ser	Gln	Leu	Tyr	Glu	Glu	Asn	Ile	Asn	Ala	Gly	Glu	Gln	Arg	
40					165					170					175		
	Ala	Leu	Ala	Leu	Arg	Ser	Glu	Ser	Ala	Ile	Glu	Ser	Gln	Gly	Ala	Gln	
				180					185					190			
45	Ile	Ser	Arg	Met	Ala	Gly	Ala	Gly	Val	Asp	Met	Ala	Pro	Asn	Ile	Phe	
			195					200					205				
	Gly	Leu	Ala	Asp	Gly	Gly	Met	His	Tyr	Gly	Ala	Ile	Ala	Tyr	Ala	Ile	
		210					215					220					
50	Ala	Asp	Gly	Ile	Glu	Leu	Ser	Ala	Ser	Ala	Lys	Met	Val	Asp	Ala	Glu	
	225					230					235					240	
	Lys	Val	Ala	Gln	Ser	Glu	Ile	Tyr	Arg	Arg	Arg	Arg	Gln	Glu	Trp	Lys	
55					245					250					255		
	Ile	Gln	Arg	Asp	Asn	Ala	Gln	Ala	Glu	Ile	Asn	Gln	Leu	Asn	Ala	Gln	
				260					265					270			
60	Leu	Glu	Ser	Leu	Ser	Ile	Arg	Arg	Glu	Ala	Ala	Glu	Met	Gln	Lys	Glu	
			275					280					285				
	Tyr	Leu	Lys	Thr	Gln	Gln	Ala	Gln	Ala	Gln	Ala	Gln	Leu	Thr	Phe	Leu	
		290					295					300					
65	Arg	Ser	Lys	Phe	Ser	Asn	Gln	Ala	Leu	Tyr	Ser	Trp	Leu	Arg	Gly	Arg	
	305					310					315				320		
	Leu	Ser	Gly	Ile	Tyr	Phe	Gln	Phe	Tyr	Asp	Leu	Ala	Val	Ser	Arg	Cys	
70					325					330					335		

Leu Met Ala Glu Gln Ser Tyr Gln Trp Glu Ala Asn Asp Asn Ser Ile
 340 345 350

5 Ser Phe Val Lys Pro Gly Ala Trp Gln Gly Thr Tyr Ala Gly Leu Leu
 355 360 365

Cys Gly Glu Ala Leu Ile Gln Asn Leu Ala Gln Met Glu Glu Ala Tyr
 370 375 380

10 Leu Lys Trp Glu Ser Arg Ala Leu Glu Val Glu Arg Thr Val Ser Leu
 385 390 395 400

15 Ala Val Val Tyr Asp Ser Leu Glu Gly Asn Asp Arg Phe Asn Leu Ala
 405 410 415

Glu Gln Ile Pro Ala Leu Leu Asp Lys Gly Glu Gly Thr Ala Gly Thr
 420 425 430

20 Lys Glu Asn Gly Leu Ser Leu Ala Asn Ala Ile Leu Ser Ala Ser Val
 435 440 445

Lys Leu Ser Asp Leu Lys Leu Gly Thr Asp Tyr Pro Asp Ser Ile Val
 450 455 460

25 Gly Ser Asn Lys Val Arg Arg Ile Lys Gln Ile Ser Val Ser Leu Pro
 465 470 475 480

30 Ala Leu Val Gly Pro Tyr Gln Asp Val Gln Ala Met Leu Ser Tyr Gly
 485 490 495

Gly Ser Thr Gln Leu Pro Lys Gly Cys Ser Ala Leu Ala Val Ser His
 500 505 510

35 Gly Thr Asn Asp Ser Gly Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys
 515 520 525

Tyr Leu Pro Phe Glu Gly Ile Ala Leu Asp Asp Gln Gly Thr Leu Asn
 530 535 540

40 Leu Gln Phe Pro Asn Ala Thr Asp Lys Gln Lys Ala Ile Leu Gln Thr
 545 550 555 560

45 Met Ser Asp Ile Ile Leu His Ile Arg Tyr Thr Ile Arg ...
 565 570 573

(2) INFORMATION FOR SEQ ID NO:56

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 2898 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56 (tcca)

60 1 ATG AAT CAA CTC GCC AGT CCC CTG ATT TCC CGC ACC GAA GAG ATC CAC 48
 1 Met Asn Gln Leu Ala Ser Pro Leu Ile Ser Arg Thr Glu Glu Ile His 16

49 AAC TTA CCC GGT AAA TTG ACC GAT CTT GGT TAT ACC TCA GTG TTT GAT 96
 65 17 Asn Leu Pro Gly Lys Leu Thr Asp Leu Gly Tyr Thr Ser Val Phe Asp 32

97 GTG GTA CGT ATG CCG CGT GAG CGT TTT ATT CGT GAG CAT CGT GCT GAT 144

	33	Val	Val	Arg	Met	Pro	Arg	Glu	Arg	Phe	Ile	Arg	Glu	His	Arg	Ala	Asp	43
5	145	CTC	GGG	CGC	AGT	GCT	GAA	AAA	ATG	TAT	GAC	CTG	GCA	GTG	GGC	TAT	GCT	192
	49	Leu	Gly	Arg	Ser	Ala	Glu	Lys	Met	Tyr	Asp	Leu	Ala	Val	Gly	Tyr	Ala	64
10	193	CAT	CAG	GTG	TTA	CAC	CAT	TTT	CGC	CGT	AAT	TCT	CTT	AGT	GAA	GCT	GTT	240
	65	His	Gln	Val	Leu	His	His	Phe	Arg	Arg	Asn	Ser	Leu	Ser	Glu	Ala	Val	30
	241	CAG	TTT	GGC	TTG	AGA	AGT	CCG	TTC	TCC	GTA	TCA	GGC	CCG	GAT	TAC	GCC	288
	81	Gln	Phe	Gly	Leu	Arg	Ser	Pro	Phe	Ser	Val	Ser	Gly	Pro	Asp	Tyr	Ala	96
15	289	AAT	CAG	TTT	CTT	GAT	GCA	AAC	ACG	GGT	TGG	AAA	GAT	AAA	GCA	CCA	AGT	336
	97	Asn	Gln	Phe	Leu	Asp	Ala	Asn	Thr	Gly	Trp	Lys	Asp	Lys	Ala	Pro	Ser	112
20	337	GGA	TCA	CCG	GAA	GCC	AAT	GAT	GCG	CCG	GTA	GCC	TAT	CTG	ACT	CAT	ATT	384
	113	Gly	Ser	Pro	Glu	Ala	Asn	Asp	Ala	Pro	Val	Ala	Tyr	Leu	Thr	His	Ile	128
25	385	TAT	CAA	TTG	GCC	CTT	GAA	CAG	GAA	AAG	AAT	GGC	GCC	ACT	ACC	ATT	ATG	432
	129	Tyr	Gln	Leu	Ala	Leu	Glu	Gln	Glu	Lys	Asn	Gly	Ala	Thr	Thr	Ile	Met	144
30	433	AAT	ACG	CTG	GCG	GAG	CGT	CGC	CCC	GAT	CTG	GGT	GCT	TTG	TTA	ATT	AAT	480
	145	Asn	Thr	Leu	Ala	Glu	Arg	Arg	Pro	Asp	Leu	Gly	Ala	Leu	Leu	Ile	Asn	160
	481	GAT	AAA	GCA	ATC	AAT	GAG	GTG	ATA	CCG	CAA	TTG	CAG	TTG	GTC	AAT	GAA	528
	161	Asp	Lys	Ala	Ile	Asn	Glu	Val	Ile	Pro	Gln	Leu	Gln	Leu	Val	Asn	Glu	176
35	529	ATT	CTG	TCC	AAA	GCT	ATT	CAG	AAG	AAA	CTG	AGT	TTG	ACT	GAT	CTG	GAA	576
	177	Ile	Leu	Ser	Lys	Ala	Ile	Gln	Lys	Lys	Leu	Ser	Leu	Thr	Asp	Leu	Glu	192
40	577	GCG	GTA	AAC	GCC	AGA	CTT	TCC	ACT	ACC	CGT	TAC	CCG	AAT	AAT	CTG	CCG	624
	193	Ala	Val	Asn	Ala	Arg	Leu	Ser	Thr	Thr	Arg	Tyr	Pro	Asn	Asn	Leu	Pro	208
45	625	TAT	CAT	TAT	GGT	CAT	CAG	CAG	ATT	CAG	ACA	GCT	CAA	TCG	GTA	TTG	GGT	672
	209	Tyr	His	Tyr	Gly	His	Gln	Gln	Ile	Gln	Thr	Ala	Gln	Ser	Val	Leu	Gly	224
50	673	ACT	ACG	TTG	CAA	GAT	ATC	ACT	TTG	CCA	CAG	ACG	CTG	GAT	CTG	CCG	CAA	720
	225	Thr	Thr	Leu	Gln	Asp	Ile	Thr	Leu	Pro	Gln	Thr	Leu	Asp	Leu	Pro	Gln	240
	721	AAC	TTC	TGG	GCA	ACA	GCA	AAA	GGA	AAA	CTG	AGC	GAT	ACG	ACT	GCC	AGT	768
	241	Asn	Phe	Trp	Ala	Thr	Ala	Lys	Gly	Lys	Leu	Ser	Asp	Thr	Thr	Ala	Ser	256
55	769	GCT	TTG	ACC	CGA	CTG	CAA	ATC	ATG	GCG	AGT	CAG	TTT	TCG	CCA	GAG	CAG	816
	257	Ala	Leu	Thr	Arg	Leu	Gln	Ile	Met	Ala	Ser	Gln	Phe	Ser	Pro	Glu	Gln	272
60	817	CAG	AAA	ATC	ATT	ACG	GAG	ACT	GTC	GGT	CAG	GAT	TTC	TAT	CAG	CTT	AAC	864
	273	Gln	Lys	Ile	Ile	Thr	Glu	Thr	Val	Gly	Gln	Asp	Phe	Tyr	Gln	Leu	Asn	288
65	865	TAT	GGT	GAC	AGT	TCG	CTT	ACT	GTG	AAT	AGT	TTC	AGC	GAC	ATG	ACC	ATA	912
	289	Tyr	Gly	Asp	Ser	Ser	Leu	Thr	Val	Asn	Ser	Phe	Ser	Asp	Met	Thr	Ile	304

	313	ATG ACT GAT CGA ACA AGT TTG ACT GTA CCC CAG GTA GAA CTG ATG TTD	360
	305	Met Thr Asp Arg Thr Ser Leu Thr Val Pro Gln Val Glu Leu Met Leu	330
5			
	951	TGT TCA ACT GTC GGA GGT TCT ACG GTT GTT AAG TCT GAT AAT GTG AGT	1003
	321	Cys Ser Thr Val Gly Gly Ser Thr Val Val Lys Ser Asp Asn Val Ser	336
10			
	1009	TCT GGT GAC ACG ACA GCG ACG CCA TTT GCG TAT GGC GCC CGC TTT ATT	1056
	337	Ser Gly Asp Thr Thr Ala Thr Pro Phe Ala Tyr Gly Ala Arg Phe Ile	352
15			
	1057	CAT GCC GGT AAG CCG GAG GCG ATT ACC CTG AGT CGC AGT GGT GCG GAG	1104
	353	His Ala Gly Lys Pro Glu Ala Ile Thr Leu Ser Arg Ser Gly Ala Glu	368
20			
	1105	GCG CAT TTT GCT CTG ACG GTT AAC AAT CTG ACA GAT GAC AAG TTG GAC	1152
	369	Ala His Phe Ala Leu Thr Val Asn Asn Leu Thr Asp Asp Lys Leu Asp	384
25			
	1153	CGT ATT AAC CGC ACA GTG CGC CTG CAA AAA TGG CTG AAT CTG CCT TAT	1200
	385	Arg Ile Asn Arg Thr Val Arg Leu Gln Lys Trp Leu Asn Leu Pro Tyr	400
30			
	1201	GAG GAT ATT GAC CTG TTA GTG ACT TCT GCT ATG GAT GCG GAA ACA GGA	1248
	401	Glu Asp Ile Asp Leu Leu Val Thr Ser Ala Met Asp Ala Glu Thr Gly	416
35			
	1249	AAT ACC GCG CTG TCG ATG AAC GAC AAT ACG CTG CGT ATG TTG GGA GTG	1296
	417	Asn Thr Ala Leu Ser Met Asn Asp Asn Thr Leu Arg Met Leu Gly Val	432
40			
	1297	TTC AAA CAT TAT CAG GCG AAG TAT GGT GTT AGC GCT AAA CAA TTT GCT	1344
	433	Phe Lys His Tyr Gln Ala Lys Tyr Gly Val Ser Ala Lys Gln Phe Ala	448
45			
	1345	GGC TCG CTG CGC GTA GTG GCC CCG TTT GCC ATT ACA CCG GCA ACG CCG	1392
	449	Gly Trp Leu Arg Val Val Ala Pro Phe Ala Ile Thr Pro Ala Thr Pro	464
50			
	1393	TTT TTA GAC CAA GTG TTT AAC TCC GTC GGC ACC TTT GAT ACA CCG TTT	1440
	465	Phe Leu Asp Gln Val Phe Asn Ser Val Gly Thr Phe Asp Thr Pro Phe	480
55			
	1441	GTG ATA GAT AAT CAG GAT TTT GTC TAT ACA TTG ACC ACC GGG GGC GAT	1488
	481	Val Ile Asp Asn Gln Asp Phe Val Tyr Thr Leu Thr Thr Gly Gly Asp	496
60			
	1489	GGG GCG CGT GTT AAG CAT ATC AGC ACG GCA CTG GGC CTC AAT CAT CGT	1536
	497	Gly Ala Arg Val Lys His Ile Ser Thr Ala Leu Gly Leu Asn His Arg	512
65			
	1537	CAG TTC CTG TTA TTG GCG GAT AAT ATT GCC CGT CAA CAG GGG AAT GTC	1584
	513	Gln Phe Leu Leu Leu Ala Asp Asn Ile Ala Arg Gln Gln Gly Asn Val	528
70			
	1585	ACG CAA AGC ACA CTC AAC TGT AAT CTG TTT GTG GTG TCA GCT TTC TAC	1632
	529	Thr Gln Ser Thr Leu Asn Cys Asn Leu Phe Val Val Ser Ala Phe Tyr	544
75			
	1633	CGT CTG GCT AAT TTG GCG CGC ACA TTG GGG ATA AAT CCA GAG TCT TTC	1680
	545	Arg Leu Ala Asn Leu Ala Arg Thr Leu Gly Ile Asn Pro Glu Ser Phe	560
80			
	1681	TGT GCC TTG GTT GAT CGA TTA GAT GCA GGT ACA GCC ATC GTC TGG CAG	1728

	551	Cys	Ala	Leu	Val	Asp	Arg	Leu	Asp	Ala	Gly	Thr	Gly	Ile	Val	Trp	Gln	574
5	1729	CAA	TTG	GCA	GGG	AAA	CCC	ACA	ATC	ACG	GTA	CCA	CAA	AAA	GAT	TCC	CCG	1776
	577	Gln	Leu	Ala	Gly	Lys	Pro	Thr	Ile	Thr	Val	Pro	Gln	Lys	Asp	Ser	Pro	590
	1777	CTG	GCG	GCG	GAT	ATT	CTG	AGT	TTG	CTG	CAA	GCG	CTA	AGT	GCG	ATT	GCT	
	1824																	
10	593	Leu	Ala	Ala	Asp	Ile	Leu	Ser	Leu	Leu	Gln	Ala	Leu	Ser	Ala	Ile	Ala	
	608																	
15	1825	CAA	TGG	CAA	CAA	CAG	CAC	GAT	TTA	GAA	TTT	TCA	GCA	CTG	CTT	TTG	CTG	1872
	609	Gln	Trp	Gln	Gln	Gln	His	Asp	Leu	Glu	Phe	Ser	Ala	Leu	Leu	Leu	Leu	624
	1873	TTG	AGT	GAC	AAC	CCT	ATT	TCT	ACC	TCG	CAG	GGC	ACT	GAC	GAT	CAA	TTG	1920
20	625	Leu	Ser	Asp	Asn	Pro	Ile	Ser	Thr	Ser	Gln	Gly	Thr	Asp	Asp	Gln	Leu	640
	1921	AAC	TTT	ATC	CGT	CAA	GTG	TGG	CAG	AAC	CTA	GGC	AGT	ACG	TTT	GTG	GGT	1958
	641	Asn	Phe	Ile	Arg	Gln	Val	Trp	Gln	Asn	Leu	Gly	Ser	Thr	Phe	Val	Gly	656
25	1969	GCA	ACA	TTG	TTG	TCC	CGC	AGT	GGG	GCA	CCA	TTA	GTC	GAT	ACC	AAC	GGC	2016
	657	Ala	Thr	Leu	Leu	Ser	Arg	Ser	Gly	Ala	Pro	Leu	Val	Asp	Thr	Asn	Gly	672
30	2017	CAC	GCT	ATT	GAC	TGG	TTT	GCT	CTG	CTC	TCA	GCA	GGT	AAT	AGT	CCG	CTT	2064
	673	His	Ala	Ile	Asp	Trp	Phe	Ala	Leu	Leu	Ser	Ala	Gly	Asn	Ser	Pro	Leu	688
35	2065	ATC	GAT	AAG	GTT	GGT	CTG	GTG	ACT	GAT	GCT	GGC	ATA	CAA	AGT	GTT	ATA	2112
	689	Ile	Asp	Lys	Val	Gly	Leu	Val	Thr	Asp	Ala	Gly	Ile	Gln	Ser	Val	Ile	704
	2113	GCA	ACG	GTG	GTC	AAT	ACA	CAA	AGC	TTA	TCT	GAT	GAA	GAT	AAG	AAG	CTG	2160
40	705	Ala	Thr	Val	Val	Asn	Thr	Gln	Ser	Leu	Ser	Asp	Glu	Asp	Lys	Lys	Leu	720
	2161	GCA	ATC	ACT	ACT	CTG	ACT	AAT	ACG	TTG	AAT	CAG	GTA	CAG	AAA	ACT	CAA	2208
	721	Ala	Ile	Thr	Thr	Leu	Thr	Asn	Thr	Leu	Asn	Gln	Val	Gln	Lys	Thr	Gln	736
45	2209	CAG	GGC	GTG	GCC	GTC	AGT	CTG	TTG	GCG	CAG	ACT	CTG	AAC	GTG	AGT	CAG	2256
	737	Gln	Gly	Val	Ala	Val	Ser	Leu	Leu	Ala	Gln	Thr	Leu	Asn	Val	Ser	Gln	752
50	2257	TCA	CTG	CCT	GCG	TTA	TTG	TTG	CGC	TGG	AGT	GGA	CAA	ACA	ACC	TAC	CAG	2304
	753	Ser	Leu	Pro	Ala	Leu	Leu	Leu	Arg	Trp	Ser	Gly	Gln	Thr	Thr	Tyr	Gln	768
55	2305	TGG	TTG	AGT	GCG	ACT	TGG	GCA	TTG	AAG	GAT	GCC	GTT	AAG	ACT	GCC	GCC	2352
	769	Trp	Leu	Ser	Ala	Thr	Trp	Ala	Leu	Lys	Asp	Ala	Val	Lys	Thr	Ala	Ala	784
	2353	GAT	ATT	CCC	GCT	GAC	TAT	CTG	CGT	CAA	TTA	CGT	GAA	GTG	GTA	CGC	CGC	2400
60	785	Asp	Ile	Pro	Ala	Asp	Tyr	Leu	Arg	Gln	Leu	Arg	Glu	Val	Val	Arg	Arg	800
	2401	TCC	TTG	TTG	ACC	CAA	CAA	TTC	ACG	CTG	AGT	CCT	GCA	ATG	GTG	CAA	ACC	2448
	801	Ser	Leu	Leu	Thr	Gln	Gln	Phe	Thr	Leu	Ser	Pro	Ala	Met	Val	Gln	Thr	816
65																		

2443 TTG CTG GAC TAT CCA GCC TAT TTT GGC GCT TCC GCA GAA ACA GTG ACC 2486
 317 Leu Leu Asp Tyr Pro Ala Tyr Phe Gly Ala Ser Ala Glu Thr Val Thr 332

5 2497 GAT ATC AGT TTG TGG ATG CTT TAT ACC CTG AGC TGT TAT AGC GAT TTA 2544
 833 Asp Ile Ser Leu Trp Met Leu Tyr Thr Leu Ser Cys Tyr Ser Asp Leu 348

10 2545 TTG CTC CAA ATG GGT GAA GCT GGT GGT ACC GAA GAT GAT GTA CTG GCC 2592
 849 Leu Leu Gln Met Gly Glu Ala Gly Gly Thr Glu Asp Asp Val Leu Ala 364

15 2593 TAC TTA CGC ACA GCT AAT GCT ACC ACA CCG TTG AGC CAA TCT GAT GCT 2640
 865 Tyr Leu Arg Thr Ala Asn Ala Thr Thr Pro Leu Ser Gln Ser Asp Ala 880

20 2641 GCA CAG ACG TTG GCA ACG CTA TTG GGT TGG GAG GTT AAC GAG TTG CAA 2688
 881 Ala Gln Thr Leu Ala Thr Leu Leu Gly Trp Glu Val Asn Glu Leu Gln 396

25 2689 GCC GCT TGG TCG GTA TTG GGC GGG ATT GCC AAA ACC ACA CCG CAA CTG 2736
 897 Ala Ala Trp Ser Val Leu Gly Gly Ile Ala Lys Thr Thr Pro Gln Leu 912

30 2737 GAT GCG CTT CTG CGT TTG CAA CAG GCA CAG AAC CAA ACT GGT CTT GGC 2784
 913 Asp Ala Leu Leu Arg Leu Gln Gln Ala Gln Asn Gln Thr Gly Leu Gly 928

35 2785 GTT ACA CAG CAA CAG CAA GGC TAT CTC CTG AGT CGT GAC AGT GAT TAT 2832
 929 Val Thr Gln Gln Gln Gln Gly Tyr Leu Leu Ser Arg Asp Ser Asp Tyr 944

2833 ACC CTT TGG CAA AGC ACC GGT CAG GCG CTG GTG GCT GGC GTA TCC CAT 2880
 945 Thr Leu Trp Gln Ser Thr Gly Gln Ala Leu Val Ala Gly Val Ser His 960

40 2881 GTC AAG GGC AGT AAC TGA 2898
 961 Val Lys Gly Ser Asn End 966

(2) INFORMATION FOR SEQ ID NO:57
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 965 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57 (TCCA peptide)

Features	From	To	Description
	1	10	SEQ ID NO:8
1	Met	Asn	Gln Leu Ala Ser Pro Leu Ile Ser Arg Thr Glu Glu Ile His 16
17	Asn	Leu	Pro Gly Lys Leu Thr Asp Leu Gly Tyr Thr Ser Val Phe Asp 32
33	Val	Val	Arg Met Pro Arg Glu Arg Phe Ile Arg Glu His Arg Ala Asp 48
49	Leu	Gly	Arg Ser Ala Glu Lys Met Tyr Asp Leu Ala Val Gly Tyr Ala 64
65	His	Gln	Val Leu His His Phe Arg Arg Asn Ser Leu Ser Glu Ala Val 80
81	Gln	Phe	Gly Leu Arg Ser Pro Phe Ser Val Ser Gly Pro Asp Tyr Ala 96

	97	Asn Gln Phe Leu Asp Ala Asn Thr Gly Trp Lys Asp Lys Ala Pro Ser	111
	113	Gly Ser Pro Glu Ala Asn Asp Ala Pro Val Ala Tyr Leu Thr His Ile	128
5	129	Tyr Gln Leu Ala Leu Glu Gln Glu Lys Asn Gly Ala Thr Thr Ile Met	144
	145	Asn Thr Leu Ala Glu Arg Arg Pro Asp Leu Gly Ala Leu Leu Ile Asn	160
10	161	Asp Lys Ala Ile Asn Glu Val Ile Pro Gln Leu Gln Leu Val Asn Glu	176
	177	Ile Leu Ser Lys Ala Ile Gln Lys Lys Leu Ser Leu Thr Asp Leu Glu	192
	193	Ala Val Asn Ala Arg Leu Ser Thr Thr Arg Tyr Pro Asn Asn Leu Pro	208
15	209	Tyr His Tyr Gly His Gln Gln Ile Gln Thr Ala Gln Ser Val Leu Gly	224
	225	Thr Thr Leu Gln Asp Ile Thr Leu Pro Gln Thr Leu Asp Leu Pro Gln	240
20	241	Asn Phe Trp Ala Thr Ala Lys Gly Lys Leu Ser Asp Thr Thr Ala Ser	256
	257	Ala Leu Thr Arg Leu Gln Ile Met Ala Ser Gln Phe Ser Pro Glu Gln	272
	273	Gln Lys Ile Ile Thr Glu Thr Val Gly Gln Asp Phe Tyr Gln Leu Asn	288
25	289	Tyr Gly Asp Ser Ser Leu Thr Val Asn Ser Phe Ser Asp Met Thr Ile	304
	305	Met Thr Asp Arg Thr Ser Leu Thr Val Pro Gln Val Glu Leu Met Leu	320
30	321	Cys Ser Thr Val Gly Gly Ser Thr Val Val Lys Ser Asp Asn Val Ser	336
	337	Ser Gly Asp Thr Thr Ala Thr Pro Phe Ala Tyr Gly Ala Arg Phe Ile	352
	353	His Ala Gly Lys Pro Glu Ala Ile Thr Leu Ser Arg Ser Gly Ala Glu	368
35	369	Ala His Phe Ala Leu Thr Val Asn Asn Leu Thr Asp Asp Lys Leu Asp	384
	385	Arg Ile Asn Arg Thr Val Arg Leu Gln Lys Trp Leu Asn Leu Pro Tyr	400
40	401	Glu Asp Ile Asp Leu Leu Val Thr Ser Ala Met Asp Ala Glu Thr Gly	416
	417	Asn Thr Ala Leu Ser Met Asn Asp Asn Thr Leu Arg Met Leu Gly Val	432
	433	Phe Lys His Tyr Gln Ala Lys Tyr Gly Val Ser Ala Lys Gln Phe Ala	448
45	449	Gly Trp Leu Arg Val Val Ala Pro Phe Ala Ile Thr Pro Ala Thr Pro	464
	465	Phe Leu Asp Gln Val Phe Asn Ser Val Gly Thr Phe Asp Thr Pro Phe	480
50	481	Val Ile Asp Asn Gln Asp Phe Val Tyr Thr Leu Thr Thr Gly Gly Asp	496
	497	Gly Ala Arg Val Lys His Ile Ser Thr Ala Leu Gly Leu Asn His Arg	512
	513	Gln Phe Leu Leu Leu Ala Asp Asn Ile Ala Arg Gln Gln Gly Asn Val	528
55	529	Thr Gln Ser Thr Leu Asn Cys Asn Leu Phe Val Val Ser Ala Phe Tyr	544
	545	Arg Leu Ala Asn Leu Ala Arg Thr Leu Gly Ile Asn Pro Glu Ser Phe	560
60	561	Cys Ala Leu Val Asp Arg Leu Asp Ala Gly Thr Gly Ile Val Trp Gln	576
	577	Gln Leu Ala Gly Lys Pro Thr Ile Thr Val Pro Gln Lys Asp Ser Pro	592
	593	Leu Ala Ala Asp Ile Leu Ser Leu Leu Gln Ala Leu Ser Ala Ile Ala	608
65	609	Gln Trp Gln Gln Gln His Asp Leu Glu Phe Ser Ala Leu Leu Leu Leu	624

525 Leu Ser Asp Asn Pro Ile Ser Thr Ser Gln Gly Thr Asp Asp Gln Leu 640
 641 Asn Phe Ile Arg Gln Val Trp Gln Asn Leu Gly Ser Thr Phe Val Gly 656
 5 657 Ala Thr Leu Leu Ser Arg Ser Gly Ala Pro Leu Val Asp Thr Asn Gly 672
 673 His Ala Ile Asp Trp Phe Ala Leu Leu Ser Ala Gly Asn Ser Pro Leu 688
 689 Ile Asp Lys Val Gly Leu Val Thr Asp Ala Gly Ile Gln Ser Val Ile 704
 10 705 Ala Thr Val Val Asn Thr Gln Ser Leu Ser Asp Glu Asp Lys Lys Leu 720
 721 Ala Ile Thr Thr Leu Thr Asn Thr Leu Asn Gln Val Gln Lys Thr Gln 736
 15 737 Gln Gly Val Ala Val Ser Leu Leu Ala Gln Thr Leu Asn Val Ser Gln 752
 753 Ser Leu Pro Ala Leu Leu Leu Arg Trp Ser Gly Gln Thr Thr Tyr Gln 768
 769 Trp Leu Ser Ala Thr Trp Ala Leu Lys Asp Ala Val Lys Thr Ala Ala 784
 20 785 Asp Ile Pro Ala Asp Tyr Leu Arg Gln Leu Arg Glu Val Val Arg Arg 800
 801 Ser Leu Leu Thr Gln Gln Phe Thr Leu Ser Pro Ala Met Val Gln Thr 816
 25 317 Leu Leu Asp Tyr Pro Ala Tyr Phe Gly Ala Ser Ala Glu Thr Val Thr 832
 833 Asp Ile Ser Leu Trp Met Leu Tyr Thr Leu Ser Cys Tyr Ser Asp Leu 848
 849 Leu Leu Gln Met Gly Glu Ala Gly Gly Thr Glu Asp Asp Val Leu Ala 864
 30 865 Tyr Leu Arg Thr Ala Asn Ala Thr Thr Pro Leu Ser Gln Ser Asp Ala 880
 881 Ala Gln Thr Leu Ala Thr Leu Leu Gly Trp Glu Val Asn Glu Leu Gln 896
 35 897 Ala Ala Trp Ser Val Leu Gly Gly Ile Ala Lys Thr Thr Pro Gln Leu 912
 913 Asp Ala Leu Leu Arg Leu Gln Gln Ala Gln Asn Gln Thr Gly Leu Gly 928
 929 Val Thr Gln Gln Gln Gln Gly Tyr Leu Leu Ser Arg Asp Ser Asp Tyr 944
 40 945 Thr Leu Trp Gln Ser Thr Gly Gln Ala Leu Val Ala Gly Val Ser His 960
 961 Val Lys Gly Ser Asn 965

45

(2) INFORMATION FOR SEQ ID NO:58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4698 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58 (tccB)

1 ATG TTA TCG ACA ATG GAA AAA CAA CTG AAT GAA TCC CAG CGT GAT GCG 43
 1 Met Leu Ser Thr Met Glu Lys Gln Leu Asn Glu Ser Gln Arg Asp Ala 16
 49 TTG GTG ACT GCC TAT ATG AAT TTT GTG GCG CCG ACG TTG AAA GGC GTC 96
 17 Leu Val Thr Gly Tyr Met Asn Phe Val Ala Pro Thr Leu Lys Gly Val 32

65

	97	AGT	GGT	CAG	CCG	GTG	ACG	GTG	GAA	GAT	TTA	TAC	GAA	TAT	TTG	CTG	ATT	144
	33	Ser	Gly	Gln	Pro	Val	Thr	Val	Glu	Asp	Leu	Tyr	Glu	Tyr	Leu	Leu	Ile	48
5	145	GAC	CCG	GAA	GTG	GCT	GAT	GAG	GTT	GAG	ACG	AGT	CGG	GTA	GCA	CAA	GCG	192
	49	Asp	Pro	Glu	Val	Ala	Asp	Glu	Val	Glu	Thr	Ser	Arg	Val	Ala	Gln	Ala	64
10	193	ATT	GCC	AGC	ATA	CAG	CAA	TAT	ATG	ACT	CGT	CTG	GTC	AAC	GGC	TCT	GAA	240
	65	Ile	Ala	Ser	Ile	Gln	Gln	Tyr	Met	Thr	Arg	Leu	Val	Asn	Gly	Ser	Glu	80
15	241	CCG	GGG	CGT	CAG	GCG	ATG	GAG	CCT	TCT	ACA	GCT	AAC	GAA	TGG	CGT	GAT	288
	81	Pro	Gly	Arg	Gln	Ala	Met	Glu	Pro	Ser	Thr	Ala	Asn	Glu	Trp	Arg	Asp	96
	289	AAT	GAT	AAC	CAA	TAT	GCT	ATC	TGG	GCT	GCG	GGG	GCT	GAG	GTT	CGA	AAT	336
	97	Asn	Asp	Asn	Gln	Tyr	Ala	Ile	Trp	Ala	Ala	Gly	Ala	Glu	Val	Arg	Asn	112
20	337	TAC	GCT	GAA	AAC	TAT	ATT	TCA	CCC	ATC	ACC	CGG	CAG	GAA	AAA	AGC	CAT	384
	113	Tyr	Ala	Glu	Asn	Tyr	Ile	Ser	Pro	Ile	Thr	Arg	Gln	Glu	Lys	Ser	His	128
25	385	TAT	TTC	TCG	GAG	CTG	GAG	ACG	ACT	TTA	AAT	CAG	AAT	CGA	CTC	GAT	CCG	432
	129	Tyr	Phe	Ser	Glu	Leu	Glu	Thr	Thr	Leu	Asn	Gln	Asn	Arg	Leu	Asp	Pro	144
30	433	GAT	CGT	GTG	CAG	GAT	GCT	GTT	TTG	GCG	TAT	CTC	AAT	GAG	TTT	GAG	GCA	480
	145	Asp	Arg	Val	Gln	Asp	Ala	Val	Leu	Ala	Tyr	Leu	Asn	Glu	Phe	Glu	Ala	160
35	481	GTG	AGT	AAT	CTA	TAT	GTG	CTC	AGT	GGT	TAT	ATT	AAT	CAG	GAT	AAA	TTT	528
	161	Val	Ser	Asn	Leu	Tyr	Val	Leu	Ser	Gly	Tyr	Ile	Asn	Gln	Asp	Lys	Phe	176
	529	GAC	CAA	GCT	ATC	TAC	TAC	TTT	ATT	GGT	CGC	ACT	ACC	ACT	AAA	CCG	TAT	576
	177	Asp	Gln	Ala	Ile	Tyr	Tyr	Phe	Ile	Gly	Arg	Thr	Thr	Thr	Lys	Pro	Tyr	192
40	577	CGC	TAC	TAC	TGG	CGT	CAG	ATG	GAT	TTG	AGT	AAG	AAC	CGT	CAA	GAT	CCG	624
	193	Arg	Tyr	Tyr	Trp	Arg	Gln	Met	Asp	Leu	Ser	Lys	Asn	Arg	Gln	Asp	Pro	208
45	625	GCA	GGG	AAT	CCG	GTG	ACG	CCA	AAT	TGC	TGG	AAT	GAT	TGG	CAG	GAA	ATC	672
	209	Ala	Gly	Asn	Pro	Val	Thr	Pro	Asn	Cys	Trp	Asn	Asp	Trp	Gln	Glu	Ile	224
50	673	ACT	TTG	CCG	CTG	TCT	GGT	GAT	ACG	GTG	CTG	GAG	CAT	ACA	GTT	CGC	CCG	720
	225	Thr	Leu	Pro	Leu	Ser	Gly	Asp	Thr	Val	Leu	Glu	His	Thr	Val	Arg	Pro	240
55	721	GTA	TTT	TAT	AAT	GAT	CGA	CTA	TAT	GTG	GCT	TGG	GTT	GAG	CGT	GAC	CCG	768
	241	Val	Phe	Tyr	Asn	Asp	Arg	Leu	Tyr	Val	Ala	Trp	Val	Glu	Arg	Asp	Pro	256
	769	GCA	GTA	CAG	AAG	GAT	GCT	GAC	GGT	AAA	AAC	ATC	GGT	AAA	ACC	CAT	GCC	816
	257	Ala	Val	Gln	Lys	Asp	Ala	Asp	Gly	Lys	Asn	Ile	Gly	Lys	Thr	His	Ala	272
60	817	TAC	AAC	ATA	AAG	TTT	GGT	TAT	AAA	CGT	TAT	GAT	GAT	ACT	TGG	ACA	GCG	864
	273	Tyr	Asn	Ile	Lys	Phe	Gly	Tyr	Lys	Arg	Tyr	Asp	Asp	Thr	Trp	Thr	Ala	288
65	865	CCG	AAT	ACG	ACC	ACG	TTA	ATG	ACA	CAA	CAA	GCA	GGG	GAA	AGT	TCA	GAA	912
	289	Pro	Asn	Thr	Thr	Thr	Leu	Met	Thr	Gln	Gln	Ala	Gly	Glu	Ser	Ser	Glu	304

5	913	ACA CAG CGA TCC AGC CTG CTG ATT GAT GAA TCT AGC ACC ACA TTG CGC	960
	305	Thr Gln Arg Ser Ser Leu Leu Ile Asp Glu Ser Ser Thr Thr Leu Arg	320
10	961	CAA GTT AAT CTG TTG GCT ACC ACC GAT TTT AGT ATC GAT CCG ACC GAG	1008
	321	Gln Val Asn Leu Leu Ala Thr Thr Asp Phe Ser Ile Asp Pro Thr Glu	336
15	1009	GAA ACG GAC AGT AAC CCG TAT GGC CGC CTA ATG TTG GCG GTG TTT CTC	1056
	337	Glu Thr Asp Ser Asn Pro Tyr Gly Arg Leu Met Leu Gly Val Phe Val	352
20	1057	CGT CAA TTT GAA GGT GAT GCG GCC AAT AGA AAA AAT AAA CCC GTT GTT	1104
	353	Arg Gln Phe Glu Gly Asp Gly Ala Asn Arg Lys Asn Lys Pro Val Val	368
25	1105	TAT GGT TAT CTC TAT TGT GAC TCA GCT TTC AAT CGT CAT GTT CTC AGG	1152
	369	Tyr Gly Tyr Leu Tyr Cys Asp Ser Ala Phe Asn Arg His Val Leu Arg	384
30	1153	CCG TTA AGT AAG AAC TTT TTG TTC AGT ACT TAC CGT GAT GAA ACG GAT	1200
	385	Pro Leu Ser Lys Asn Phe Leu Phe Ser Thr Tyr Arg Asp Glu Thr Asp	400
35	1201	GGT CAA AAC AGC TTG CAA TTT GCG GTA TAC GAT AAA AAG TAT GTA ATT	1248
	401	Gly Gln Asn Ser Leu Gln Phe Ala Val Tyr Asp Lys Lys Tyr Val Ile	416
40	1249	ACT AAG GTT GTT ACA GGT GCA ACG GAA GAT CCC GAA AAT ACA GGA TGG	1296
	417	Thr Lys Val Val Thr Gly Ala Thr Glu Asp Pro Glu Asn Thr Gly Trp	432
45	1297	GTA AGT AAA GTT GAT GAC TTG AAA CAA GGC ACT ACT GGG GCC TAT GTG	1344
	433	Val Ser Lys Val Asp Asp Leu Lys Gln Gly Thr Thr Gly Ala Tyr Val	448
50	1345	TAT ATC GAT CAA GAT GGC CTG ACG CTT CAT ATA CAA ACC ACA ACT AAT	1392
	449	Tyr Ile Asp Gln Asp Gly Leu Thr Leu His Ile Gln Thr Thr Thr Asn	464
55	1393	GGG GAT TTT ATT AAC CGT CAT ACG TTT GGA TAT AAC GAT CTT GTA TAT	1440
	465	Gly Asp Phe Ile Asn Arg His Thr Phe Gly Tyr Asn Asp Leu Val Tyr	480
60	1441	GAT TCT AAG TCT GGT TAT GGT TTC ACG TCG TCA GGA AAT GAA GGT TTT	1488
	481	Asp Ser Lys Ser Gly Tyr Gly Phe Thr Trp Ser Gly Asn Glu Gly Phe	496
65	1489	TAT CTG GAT TAC CAT GAT GGA AAT TAT TAC ACC TTT CAT AAT GCA ATA	1536
	497	Tyr Leu Asp Tyr His Asp Gly Asn Tyr Tyr Thr Phe His Asn Ala Ile	512
70	1537	ATC AAC TAC TAT CCG TCT GGA TAT GGT GGT GGA TCT GTT CCT AAT GGA	1584
	513	Ile Asn Tyr Tyr Pro Ser Gly Tyr Gly Gly Ser Val Pro Asn Gly	523
75	1585	ACG TCG GCG TTA GAG CAA AGG ATT AAT GAG GGA TGG GCT ATT GCT CCC	1632
	529	Thr Trp Ala Leu Glu Gln Arg Ile Asn Glu Gly Trp Ala Ile Ala Pro	544
80	1633	CTG CTT GAT ACT CTC CAT ACT GTT ACT GTG AAG GGC AGT TAT ATC GCT	1680
	545	Leu Leu Asp Thr Leu His Thr Val Thr Val Lys Gly Ser Tyr Ile Ala	560

	1631	TGG GAA GGG GAA ACA CCT ACC GGT TAT AAT CTG TAT ATT CCA GAT GGT	1728
	561	Trp Glu Gly Glu Thr Pro Thr Gly Tyr Asn Leu Tyr Ile Pro Asp Gly	576
5	1729	ACC CTG TTG CTA GAT TGG TTT GAT AAA ATA AAT TTT GCT ATT GGT CTT	1776
	577	Thr Val Leu Leu Asp Trp Phe Asp Lys Ile Asn Phe Ala Ile Gly Leu	592
10	1777	AAT AAG CTT GAG TCT GTA TTT ACG TCG CCA GAT TGG CCA ACA CTA ACC	1824
	593	Asn Lys Leu Glu Ser Val Phe Thr Ser Pro Asp Trp Pro Thr Leu Thr	608
15	1825	ACT ATC AAA AAT TTC AGT AAA ATC GCC GAT AAC CGC AAA TTC TAT CAG	1872
	609	Thr Ile Lys Asn Phe Ser Lys Ile Ala Asp Asn Arg Lys Phe Tyr Gln	624
	1873	GAA ATC AAT GCT GAG ACG GCG GAT GGA CGC AAC CTG TTT AAA CGT TAC	1920
	625	Glu Ile Asn Ala Glu Thr Ala Asp Gly Arg Asn Leu Phe Lys Arg Tyr	640
20	1921	AGT ACT CAA ACT TTC GGA CTT ACC AGC GGT GCG ACT TAT TCT ACA ACT	1968
	641	Ser Thr Gln Thr Phe Gly Leu Thr Ser Gly Ala Thr Tyr Ser Thr Thr	656
25	1969	TAT ACT TTG TCT GAG GCG GAT TTC TCC ACT GAT CCG GAC AAA AAC TAC	2016
	657	Tyr Thr Leu Ser Glu Ala Asp Phe Ser Thr Asp Pro Asp Lys Asn Tyr	672
30	2017	CTA CAG GTT TGT TTG AAT GTC GTG TGG GAT CAT TAT GAC CGC CCG TCA	2064
	673	Leu Gln Val Cys Leu Asn Val Val Trp Asp His Tyr Asp Arg Pro Ser	688
35	2065	GGG AAA AAA GGG GCT TAT TCT TGG GTC AGT AAG TGG TTT AAC GTC TAT	2112
	689	Gly Lys Lys Gly Ala Tyr Ser Trp Val Ser Lys Trp Phe Asn Val Tyr	704
	2113	GTT GCG TTG CAA GAT AGC AAA GCT CCG GAT GCC ATT CCT CGA TTA GTT	2160
	705	Val Ala Leu Gln Asp Ser Lys Ala Pro Asp Ala Ile Pro Arg Leu Val	720
40	2161	TCC CGT TAC GAT AGT AAA CGT GGT CTG GTG CAA TAT CTG GAC TTC TGG	2208
	721	Ser Arg Tyr Asp Ser Lys Arg Gly Leu Val Gln Tyr Leu Asp Phe Trp	736
45	2209	ACC TCA TCA TTA CCC GCG AAA ACC CGT CTT AAC ACC ACC TTT GTG CGT	2256
	737	Thr Ser Ser Leu Pro Ala Lys Thr Arg Leu Asn Thr Thr Phe Val Arg	752
50	2257	ACT TTG ATT GAG AAG GCT AAT CTG GGG CTG GAT AGT TTG CTG GAT TAC	2304
	753	Thr Leu Ile Glu Lys Ala Asn Leu Gly Leu Asp Ser Leu Leu Asp Tyr	768
55	2305	ACC TTG CAG GCA GAT CCT TCT CTG GAA GCA GAT TTA GTG ACT GAC GGC	2352
	769	Thr Leu Gln Ala Asp Pro Ser Leu Glu Ala Asp Leu Val Thr Asp Gly	784
	2353	AAA AGC GAA CCA ATG GAC TTT AAT GGT TCA AAC GGT CTC TAT TTC TGG	2400
	785	Lys Ser Glu Pro Met Asp Phe Asn Gly Ser Asn Gly Leu Tyr Phe Trp	300
60	2401	GAA TTG TTC TTT CAC CTG CCG TTT TTG GTT GCT ACA CGC TTT GCC AAC	2448
	801	Glu Leu Phe Phe His Leu Pro Phe Leu Val Ala Thr Arg Phe Ala Asn	316
65	2449	GAA CAG CAA TTT TCG CCG GCA CAA AAG AGT TTG CAT TAC ATC TTT GAC	2496
	817	Glu Gln Gln Phe Ser Pro Ala Gln Lys Ser Leu His Tyr Ile Phe Asp	332

5	2497	CCG GCG ATG AAA AAC AAG CCA CAC AAT GCC CCG GCT TAT TCG AAT GTA	2544
	333	Pro Ala Met Lys Asn Lys Pro His Asn Ala Pro Ala Tyr Trp Asn Val	348
10	2545	CGT CCG TTG GTT GAA GGA AAC AGC GAT TTG TCA CGT CAT TTG GAC GAT	2592
	349	Arg Pro Leu Val Glu Gly Asn Ser Asp Leu Ser Arg His Leu Asp Asp	364
15	2593	TCT ATA GAC CCA GAT ACT CAA GCT TAT GCT CAT CCG GTG ATA TAC CAG	2640
	365	Ser Ile Asp Pro Asp Thr Gln Ala Tyr Ala His Pro Val Ile Tyr Gln	380
20	2641	AAA GCG GTG TTT ATT GCC TAT GTC AGT AAC CTG ATT GCT CAG GGA GAT	2688
	381	Lys Ala Val Phe Ile Ala Tyr Val Ser Asn Leu Ile Ala Gln Gly Asp	396
25	2689	ATG TGG TAT CGC CAA TTG ACT CGT GAC GGT CTG ACT CAG GCC CGT GTC	2736
	397	Met Trp Tyr Arg Gln Leu Thr Arg Asp Gly Leu Thr Gln Ala Arg Val	312
30	2737	TAT TAC AAT CTG GCC GCT GAA TTG CTA GGG CCT CGT CCG GAT GTA TCG	2784
	913	Tyr Tyr Asn Leu Ala Ala Glu Leu Leu Gly Pro Arg Pro Asp Val Ser	928
35	2785	CTG AGT AGC ATT TGG ACG CCG CAA ACC CTG GAT ACC TTA GCA GCC GGG	2832
	929	Leu Ser Ser Ile Trp Thr Pro Gln Thr Leu Asp Thr Leu Ala Ala Gly	944
40	2833	CAA AAA GCG GTT TTA CGT GAT TTT GAG CAC CAG TTG GCT AAT AGT GAT	2880
	945	Gln Lys Ala Val Leu Arg Asp Phe Glu His Gln Leu Ala Asn Ser Asp	960
45	2881	ACC GCT TTA CCC GCA TTG CCG GGC CGC AAT GTC AGC TAC TTG AAA CTG	2928
	961	Thr Ala Leu Pro Ala Leu Pro Gly Arg Asn Val Ser Tyr Leu Lys Leu	976
50	2929	GCA GAT AAT GGC TAC TTT AAT GAA CCG CTC AAT GTT CTG ATG TTG TCT	2976
	977	Ala Asp Asn Gly Tyr Phe Asn Glu Pro Leu Asn Val Leu Met Leu Ser	992
55	2977	CAC TGG GAT ACG TTG GAT GCA CCG TTA TAC AAT CTG CGT CAT AAC CTC	3024
	993	His Trp Asp Thr Leu Asp Ala Arg Leu Tyr Asn Leu Arg His Asn Leu	1008
60	3025	ACC GTT GAT GGC AAG CCG CTT TCG CTG CCG CTG TAT GCT GCG CCT GTT	3072
	1009	Thr Val Asp Gly Lys Pro Leu Ser Leu Pro Leu Tyr Ala Ala Pro Val	1024
65	3073	GAT CCG GTA GCG TTG TTG GCT CAG CGT GCT CAG TCC GCG ACG TTG ACG	3120
	1025	Asp Pro Val Ala Leu Leu Ala Gln Arg Ala Gln Ser Gly Thr Leu Thr	1040
70	3121	AAT GGC GTC AGT GGC GCC ATG TTG ACG GTG CCG CCA TAC CGT TTC AGC	3168
	1041	Asn Gly Val Ser Gly Ala Met Leu Thr Val Pro Pro Tyr Arg Phe Ser	1056
75	3169	GCT ATG TTG CCG CGA GCT TAC AGC GCC GTG GGT ACG TTG ACC AGT TTT	3216
	1057	Ala Met Leu Pro Arg Ala Tyr Ser Ala Val Gly Thr Leu Thr Ser Phe	1072
80	3217	GGT CAG AAC CTG CTT AGT TTG TTG GAA CGT AGC GAA CGA GCC TGT CAA	3264
	1073	Gly Gln Asn Leu Leu Ser Leu Leu Glu Arg Ser Glu Arg Ala Cys Gln	1088

	3265	GAA GAG TTG GCG CAA CAG CAA CTG TTG GAT ATG TCC AGC TAT GCG ATC	3311
	1089	Glu Glu Leu Ala Gln Gln Gln Leu Leu Asp Met Ser Ser Tyr Ala Ile	1104
5	3313	ACG TTG CAA CAA CAG GCG CTG GAT GGA TTG GCG GCA GAT CGT CTG GCG	3360
	1105	Thr Leu Gln Gln Gln Ala Leu Asp Gly Leu Ala Ala Asp Arg Leu Ala	1120
10	3361	CTG CTA GCT AGT CAG GCT ACG GCA CAA CAG CGT CAT GAC CAT TAT TAC	3403
	1121	Leu Leu Ala Ser Gln Ala Thr Ala Gln Gln Arg His Asp His Tyr Tyr	1156
15	3409	ACT CTG TAT CAG AAC AAC ATC TCC AGT GCG GAA CAA CTG GTG ATG GAC	3456
	1137	Thr Leu Tyr Gln Asn Asn Ile Ser Ser Ala Glu Gln Leu Val Met Asp	1152
	3457	ACC CAA ACG TCA GCA CAA TCC CTG ATT TCT TCT TCC ACT GGT GTA CAA	3504
	1153	Thr Gln Thr Ser Ala Gln Ser Leu Ile Ser Ser Ser Thr Gly Val Gln	1168
20	3505	ACT GCC AGT GGG GCA CTG AAA GTG ATC CCG AAT ATC TTT GGT TTG GCT	3552
	1169	Thr Ala Ser Gly Ala Leu Lys Val Ile Pro Asn Ile Phe Gly Leu Ala	1134
25	3553	GAT GGC GGC TCG CGC TAT GAA GGA GTA ACG GAA GCG ATT GCC ATC GGG	3600
	1185	Asp Gly Gly Ser Arg Tyr Glu Gly Val Thr Glu Ala Ile Ala Ile Gly	1200
30	3601	TTA ATG GCT GCC GGA CAA GCC ACC AGC GTG GTG GCC GAG CGT CTG GCA	3648
	1201	Leu Met Ala Ala Gly Gln Ala Thr Ser Val Val Ala Glu Arg Leu Ala	1216
35	3649	ACC ACG GAG AAT TAC CGC CGC CGC CGT GAA GAG TGG CAA ATC CAA TAC	3696
	1217	Thr Thr Glu Asn Tyr Arg Arg Arg Arg Glu Glu Trp Gln Ile Gln Tyr	1232
	3697	CAG CAG GCA CAG TCT GAG GTC GAC GCA TTA CAG AAA CAG TTG GAT GCG	3744
	1233	Gln Gln Ala Gln Ser Glu Val Asp Ala Leu Gln Lys Gln Leu Asp Ala	1248
40	3745	CTG GCA GTG CGC GAG AAA GCA GCT CAA ACT TCC CTG CAA CAG GCG AAG	3792
	1249	Leu Ala Val Arg Glu Lys Ala Ala Gln Thr Ser Leu Gln Gln Ala Lys	1264
45	3793	GCA CAG CAG GTA CAA ATT CGG ACC ATG CTG ACT TAC TTA ACT ACT CGT	3840
	1265	Ala Gln Gln Val Gln Ile Arg Thr Met Leu Thr Tyr Leu Thr Thr Arg	1280
50	3841	TTC ACC CAG GCG ACT CTG TAC CAG TGG CTG AGT GGT CAA TTA TCC GCG	3888
	1281	Phe Thr Gln Ala Thr Leu Tyr Gln Trp Leu Ser Gly Gln Leu Ser Ala	1296
55	3889	TTG TAT TAT CAA GCG TAT GAT GCC GTG GTT GCT CTC TGC CTC TCC GCC	3936
	1297	Leu Tyr Tyr Gln Ala Tyr Asp Ala Val Val Ala Leu Cys Leu Ser Ala	1312
	3937	CAA GCT TGC TGG CAG TAT GAA TTG GGT GAT TAC GCT ACC ACT TTT ATC	3984
	1313	Gln Ala Cys Trp Gln Tyr Glu Leu Gly Asp Tyr Ala Thr Thr Phe Ile	1323
60	3985	CAG ACC GGT ACC TGG AAC GAC CAT TAC CGT GGT TTG CAA GTG GCG GAG	4032
	1329	Gln Thr Gly Thr Trp Asn Asp His Tyr Arg Gly Leu Gln Val Gly Glu	1344
65	4033	ACA CTG CAA CTC AAT TTG CAT CAG ATG GAA GCG GCC TAT TTA GTT CGT	4080
	1345	Thr Leu Gln Leu Asn Leu His Gln Met Glu Ala Ala Tyr Leu Val Arg	1360

5
4081 CAC GAA CGC CGT CTT AAT GTG ATC CGT ACT GTG TCG CTC AAA AGC CTA 4128
1361 His Glu Arg Arg Leu Asn Val Ile Arg Thr Val Ser Leu Lys Ser Leu 1376

10
4129 TTG GGT GAT GAT GGT TTT GGT AAG TTA AAA ACC GAA GGC AAA GTC GAC 4176
1377 Leu Gly Asp Asp Gly Phe Gly Lys Leu Lys Thr Glu Gly Lys Val Asp 1392

15
4177 TTT CCA TTA AGC GAA AAG CTG TTT GAC AAC GAC TAT CCG GGG CAC TAT 4224
1393 Phe Pro Leu Ser Glu Lys Leu Phe Asp Asn Asp Tyr Pro Gly His Tyr 1408

20
4225 TTG CGC CAG ATT AAA ACT GTG TCA GTG ACG TTG CCG ACG TTA GTC GGG 4272
1409 Leu Arg Gln Ile Lys Thr Val Ser Val Thr Leu Pro Thr Leu Val Gly 1424

25
4273 CCG TAT CAA AAC GTG AAG GCA ACG CTC ACT CAG ACC AGC AGC AGT ATA 4320
1425 Pro Tyr Gln Asn Val Lys Ala Thr Leu Thr Gln Thr Ser Ser Ser Ile 1440

30
4321 TTG TTA GCA GCA GAT ATC AAT GGT GTT AAA CGT CTC AAT GAT CCG ACA 4368
1441 Leu Leu Ala Ala Asp Ile Asn Gly Val Lys Arg Leu Asn Asp Pro Thr 1456

35
4369 GGT AAA GAG GGT GAT GCG ACG CAT ATT GTC ACC AAT CTG CGT GCC AGC 4416
1457 Gly Lys Glu Gly Asp Ala Thr His Ile Val Thr Asn Leu Arg Ala Ser 1472

40
4417 CAG CAG GTG GCG CTC TCT TCT GGC ATT AAT GAT GCC GGT AGC TTT GAG 4464
1473 Gln Gln Val Ala Leu Ser Ser Gly Ile Asn Asp Ala Gly Ser Phe Glu 1488

45
4465 TTG CGT TTG GAA GAT GAG CGC TAT CTA TCA TTT GAG GGG ACT GGA GCT 4512
1489 Leu Arg Leu Glu Asp Glu Arg Tyr Leu Ser Phe Glu Gly Thr Gly Ala 1504

50
4513 GTT TCC AAA TCG ACT CTT AAC TTC CCG CGT TCT GTG GAT GAG CAT ATT 4560
1505 Val Ser Lys Trp Thr Leu Asn Phe Pro Arg Ser Val Asp Glu His Ile 1520

55
4561 GAC GAT AAG ACA TTG AAA GCG GAT GAG ATG CAG GCC GCA CTG TTG GCG 4608
1521 Asp Asp Lys Thr Leu Lys Ala Asp Glu Met Gln Ala Ala Leu Leu Ala 1536

60
4609 AAT ATG GAT GAT GTG CTG GTG CAG GTG CAT TAT ACC GCC TCC GAC GGC 4656
1537 Asn Met Asp Asp Val Leu Val Gln Val His Tyr Thr Ala Cys Asp Gly 1552

65
4657 GGC GCC AGT TTC GCA AAC CAG GTC AAG AAA ACA CTC TCT TAA 4698
1553 Gly Ala Ser Phe Ala Asn Gln Val Lys Lys Thr Leu Ser End 1566

55 (2) INFORMATION FOR SEQ ID NO:59
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1665 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59 (TccB peptide)
Features From To Description

i 11 SEQ ID NO:7

5	1	Met Leu Ser Thr Met Glu Lys Gln Leu Asn Glu Ser Gln Arg Asp Ala	16
	17	Leu Val Thr Gly Tyr Met Asn Phe Val Ala Pro Thr Leu Lys Gly Val	32
	33	Ser Gly Gln Pro Val Thr Val Glu Asp Leu Tyr Glu Tyr Leu Leu Ile	48
10	49	Asp Pro Glu Val Ala Asp Glu Val Glu Thr Ser Arg Val Ala Gln Ala	64
	65	Ile Ala Ser Ile Gln Gln Tyr Met Thr Arg Leu Val Asn Gly Ser Glu	80
15	81	Pro Gly Arg Gln Ala Met Glu Pro Ser Thr Ala Asn Glu Trp Arg Asp	96
	97	Asn Asp Asn Gln Tyr Ala Ile Trp Ala Ala Gly Ala Glu Val Arg Asn	112
	113	Tyr Ala Glu Asn Tyr Ile Ser Pro Ile Thr Arg Gln Glu Lys Ser His	128
20	129	Tyr Phe Ser Glu Leu Glu Thr Thr Leu Asn Gln Asn Arg Leu Asp Pro	144
	145	Asp Arg Val Gln Asp Ala Val Leu Ala Tyr Leu Asn Glu Phe Glu Ala	160
25	161	Val Ser Asn Leu Tyr Val Leu Ser Gly Tyr Ile Asn Gln Asp Lys Phe	176
	177	Asp Gln Ala Ile Tyr Tyr Phe Ile Gly Arg Thr Thr Thr Lys Pro Tyr	192
	193	Arg Tyr Tyr Trp Arg Gln Met Asp Leu Ser Lys Asn Arg Gln Asp Pro	208
30	209	Ala Gly Asn Pro Val Thr Pro Asn Cys Trp Asn Asp Trp Gln Glu Ile	224
	225	Thr Leu Pro Leu Ser Gly Asp Thr Val Leu Glu His Thr Val Arg Pro	240
35	241	Val Phe Tyr Asn Asp Arg Leu Tyr Val Ala Trp Val Glu Arg Asp Pro	256
	257	Ala Val Gln Lys Asp Ala Asp Gly Lys Asn Ile Gly Lys Thr His Ala	272
	273	Tyr Asn Ile Lys Phe Gly Tyr Lys Arg Tyr Asp Asp Thr Trp Thr Ala	288
40	289	Pro Asn Thr Thr Thr Leu Met Thr Gln Gln Ala Gly Glu Ser Ser Glu	304
	305	Thr Gln Arg Ser Ser Leu Leu Ile Asp Glu Ser Ser Thr Thr Leu Arg	320
45	321	Gln Val Asn Leu Leu Ala Thr Thr Asp Phe Ser Ile Asp Pro Thr Glu	336
	337	Glu Thr Asp Ser Asn Pro Tyr Gly Arg Leu Met Leu Gly Val Phe Val	352
	353	Arg Gln Phe Glu Gly Asp Gly Ala Asn Arg Lys Asn Lys Pro Val Val	368
50	369	Tyr Gly Tyr Leu Tyr Cys Asp Ser Ala Phe Asn Arg His Val Leu Arg	384
	385	Pro Leu Ser Lys Asn Phe Leu Phe Ser Thr Tyr Arg Asp Glu Thr Asp	400
55	401	Gly Gln Asn Ser Leu Gln Phe Ala Val Tyr Asp Lys Lys Tyr Val Ile	416
	417	Thr Lys Val Val Thr Gly Ala Thr Glu Asp Pro Glu Asn Thr Gly Trp	432
	433	Val Ser Lys Val Asp Asp Leu Lys Gln Gly Thr Thr Gly Ala Tyr Val	448
60	449	Tyr Ile Asp Gln Asp Gly Leu Thr Leu His Ile Gln Thr Thr Thr Asn	464
	465	Gly Asp Phe Ile Asn Arg His Thr Phe Gly Tyr Asn Asp Leu Val Tyr	480
65	481	Asp Ser Lys Ser Gly Tyr Gly Phe Thr Trp Ser Gly Asn Glu Gly Phe	496
	497	Tyr Leu Asp Tyr His Asp Gly Asn Tyr Tyr Thr Phe His Asn Ala Ile	512

	513	Ile Asn Tyr Tyr Pro Ser Gly Tyr Gly Gly Gly Ser Val Pro Asn Gly	523
5	529	Thr Trp Ala Leu Glu Gln Arg Ile Asn Glu Gly Trp Ala Ile Ala Pro	544
	545	Leu Leu Asp Thr Leu His Thr Val Thr Val Lys Gly Ser Tyr Ile Ala	560
	561	Trp Glu Gly Glu Thr Pro Thr Gly Tyr Asn Leu Tyr Ile Pro Asp Gly	576
10	577	Thr Val Leu Leu Asp Trp Phe Asp Lys Ile Asn Phe Ala Ile Gly Leu	592
	593	Asn Lys Leu Glu Ser Val Phe Thr Ser Pro Asp Trp Pro Thr Leu Thr	608
15	609	Thr Ile Lys Asn Phe Ser Lys Ile Ala Asp Asn Arg Lys Phe Tyr Gln	624
	625	Glu Ile Asn Ala Glu Thr Ala Asp Gly Arg Asn Leu Phe Lys Arg Tyr	640
	641	Ser Thr Gln Thr Phe Gly Leu Thr Ser Gly Ala Thr Tyr Ser Thr Thr	656
20	657	Tyr Thr Leu Ser Glu Ala Asp Phe Ser Thr Asp Pro Asp Lys Asn Tyr	672
	673	Leu Gln Val Cys Leu Asn Val Val Trp Asp His Tyr Asp Arg Pro Ser	688
25	689	Gly Lys Lys Gly Ala Tyr Ser Trp Val Ser Lys Trp Phe Asn Val Tyr	704
	705	Val Ala Leu Gln Asp Ser Lys Ala Pro Asp Ala Ile Pro Arg Leu Val	720
	721	Ser Arg Tyr Asp Ser Lys Arg Gly Leu Val Gln Tyr Leu Asp Phe Trp	736
30	737	Thr Ser Ser Leu Pro Ala Lys Thr Arg Leu Asn Thr Thr Phe Val Arg	752
	753	Thr Leu Ile Glu Lys Ala Asn Leu Gly Leu Asp Ser Leu Leu Asp Tyr	768
35	769	Thr Leu Gln Ala Asp Pro Ser Leu Glu Ala Asp Leu Val Thr Asp Gly	784
	785	Lys Ser Glu Pro Met Asp Phe Asn Gly Ser Asn Gly Leu Tyr Phe Trp	800
	801	Glu Leu Phe Phe His Leu Pro Phe Leu Val Ala Thr Arg Phe Ala Asn	816
40	817	Glu Gln Gln Phe Ser Pro Ala Gln Lys Ser Leu His Tyr Ile Phe Asp	832
	833	Pro Ala Met Lys Asn Lys Pro His Asn Ala Pro Ala Tyr Trp Asn Val	848
45	849	Arg Pro Leu Val Glu Gly Asn Ser Asp Leu Ser Arg His Leu Asp Asp	864
	865	Ser Ile Asp Pro Asp Thr Gln Ala Tyr Ala His Pro Val Ile Tyr Gln	880
	881	Lys Ala Val Phe Ile Ala Tyr Val Ser Asn Leu Ile Ala Gln Gly Asp	896
50	897	Met Trp Tyr Arg Gln Leu Thr Arg Asp Gly Leu Thr Gln Ala Arg Val	912
	913	Tyr Tyr Asn Leu Ala Ala Glu Leu Leu Gly Pro Arg Pro Asp Val Ser	928
55	929	Leu Ser Ser Ile Trp Thr Pro Gln Thr Leu Asp Thr Leu Ala Ala Gly	944
	945	Gln Lys Ala Val Leu Arg Asp Phe Glu His Gln Leu Ala Asn Ser Asp	960
	961	Thr Ala Leu Pro Ala Leu Pro Gly Arg Asn Val Ser Tyr Leu Lys Leu	976
60	977	Ala Asp Asn Gly Tyr Phe Asn Glu Pro Leu Asn Val Leu Met Leu Ser	992
	993	His Trp Asp Thr Leu Asp Ala Arg Leu Tyr Asn Leu Arg His Asn Leu	1008
65	1009	Thr Val Asp Gly Lys Pro Leu Ser Leu Pro Leu Tyr Ala Ala Pro Val	1024
	1025	Asp Pro Val Ala Leu Leu Ala Gln Arg Ala Gln Ser Gly Thr Leu Thr	1040

	1041	Asn Gly Val Ser Gly Ala Met Leu Thr Val Pro Pro Tyr Arg Phe Ser	1056
	1057	Ala Met Leu Pro Arg Ala Tyr Ser Ala Val Gly Thr Leu Thr Ser Phe	1072
5	1073	Gly Gln Asn Leu Leu Ser Leu Leu Glu Arg Ser Glu Arg Ala Cys Gln	1088
	1089	Glu Glu Leu Ala Gln Gln Gln Leu Leu Asp Met Ser Ser Tyr Ala Ile	1104
10	1105	Thr Leu Gln Gln Gln Ala Leu Asp Gly Leu Ala Ala Asp Arg Leu Ala	1120
	1121	Leu Leu Ala Ser Gln Ala Thr Ala Gln Gln Arg His Asp His Tyr Tyr	1136
	1137	Thr Leu Tyr Gln Asn Asn Ile Ser Ser Ala Glu Gln Leu Val Met Asp	1152
15	1153	Thr Gln Thr Ser Ala Gln Ser Leu Ile Ser Ser Ser Thr Gly Val Gln	1168
	1169	Thr Ala Ser Gly Ala Leu Lys Val Ile Pro Asn Ile Phe Gly Leu Ala	1184
20	1185	Asp Gly Gly Ser Arg Tyr Glu Gly Val Thr Glu Ala Ile Ala Ile Gly	1200
	1201	Leu Met Ala Ala Gly Gln Ala Thr Ser Val Val Ala Glu Arg Leu Ala	1216
	1217	Thr Thr Glu Asn Tyr Arg Arg Arg Arg Glu Glu Trp Gln Ile Gln Tyr	1232
25	1233	Gln Gln Ala Gln Ser Glu Val Asp Ala Leu Gln Lys Gln Leu Asp Ala	1248
	1249	Leu Ala Val Arg Glu Lys Ala Ala Gln Thr Ser Leu Gln Gln Ala Lys	1264
30	1265	Ala Gln Gln Val Gln Ile Arg Thr Met Leu Thr Tyr Leu Thr Thr Arg	1280
	1281	Phe Thr Gln Ala Thr Leu Tyr Gln Trp Leu Ser Gly Gln Leu Ser Ala	1296
	1297	Leu Tyr Tyr Gln Ala Tyr Asp Ala Val Val Ala Leu Cys Leu Ser Ala	1312
35	1313	Gln Ala Cys Trp Gln Tyr Glu Leu Gly Asp Tyr Ala Thr Thr Phe Ile	1328
	1329	Gln Thr Gly Thr Trp Asn Asp His Tyr Arg Gly Leu Gln Val Gly Glu	1344
40	1345	Thr Leu Gln Leu Asn Leu His Gln Met Glu Ala Ala Tyr Leu Val Arg	1360
	1361	His Glu Arg Arg Leu Asn Val Ile Arg Thr Val Ser Leu Lys Ser Leu	1376
	1377	Leu Gly Asp Asp Gly Phe Gly Lys Leu Lys Thr Glu Gly Lys Val Asp	1392
45	1393	Phe Pro Leu Ser Glu Lys Leu Phe Asp Asn Asp Tyr Pro Gly His Tyr	1408
	1409	Leu Arg Gln Ile Lys Thr Val Ser Val Thr Leu Pro Thr Leu Val Gly	1424
50	1425	Pro Tyr Gln Asn Val Lys Ala Thr Leu Thr Gln Thr Ser Ser Ser Ile	1440
	1441	Leu Leu Ala Ala Asp Ile Asn Gly Val Lys Arg Leu Asn Asp Pro Thr	1456
	1457	Gly Lys Glu Gly Asp Ala Thr His Ile Val Thr Asn Leu Arg Ala Ser	1472
55	1473	Gln Gln Val Ala Leu Ser Ser Gly Ile Asn Asp Ala Gly Ser Phe Glu	1488
	1489	Leu Arg Leu Glu Asp Glu Arg Tyr Leu Ser Phe Glu Gly Thr Gly Ala	1504
60	1505	Val Ser Lys Trp Thr Leu Asn Phe Pro Arg Ser Val Asp Glu His Ile	1520
	1521	Asp Asp Lys Thr Leu Lys Ala Asp Glu Met Gln Ala Ala Leu Leu Ala	1536
	1537	Asn Met Asp Asp Val Leu Val Gln Val His Tyr Thr Ala Cys Asp Gly	1552
65	1553	Gly Ala Ser Phe Ala Asn Gln Val Lys Lys Thr Leu Ser	1565

(2) INFORMATION FOR SEQ ID NO:60

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 3132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60 (CCCC)

15 1 ATG AGT CCG TCT GAG ACT ACT CTT TAT ACT CAA ACC CCA ACA GTC AGC 48
 1 Met Ser Pro Ser Glu Thr Thr Leu Tyr Thr Gln Thr Pro Thr Val Ser 16

20 49 GTG TTA GAT AAT CGC GGT CTG TCC ATT CGT GAT ATT GGT TTT CAC CGT 96
 17 Val Leu Asp Asn Arg Gly Leu Ser Ile Arg Asp Ile Gly Phe His Arg 32

25 97 ATT GTA ATC GGG GGG GAT ACT GAC ACC CGC GTC ACC CGT CAC CAG TAT 144
 33 Ile Val Ile Gly Gly Asp Thr Asp Thr Arg Val Thr Arg His Gln Tyr 48

145 GAT GCC CGT GGA CAC CTG AAC TAC AGT ATT GAC CCA CGC TTG TAT GAT 192
 49 Asp Ala Arg Gly His Leu Asn Tyr Ser Ile Asp Pro Arg Leu Tyr Asp 64

30 193 GCA AAG CAG GCT GAT AAC TCA GTA AAG CCT AAT TTT GTC TGG CAG CAT 240
 65 Ala Lys Gln Ala Asp Asn Ser Val Lys Pro Asn Phe Val Trp Gln His 80

35 241 GAT CTG GCC GGT CAT GCC CTG CGG ACA GAG AGT GTC GAT GCT GGT CGT 288
 81 Asp Leu Ala Gly His Ala Leu Arg Thr Glu Ser Val Asp Ala Gly Arg 96

40 289 ACT GTT GCA TTG AAT GAT ATT GAA GGT CGT TCG GTA ATG ACA ATG AAT 336
 97 Thr Val Ala Leu Asn Asp Ile Glu Gly Arg Ser Val Met Thr Met Asn 112

45 337 GCG ACC GGT GTT CGT CAG ACC CGT CGC TAT GAA GGC AAC ACC TTG CCC 384
 113 Ala Thr Gly Val Arg Gln Thr Arg Arg Tyr Glu Gly Asn Thr Leu Pro 128

50 385 GGT CGC TTG TTA TCT GTG AGC GAG CAA GTT TTC AAC CAA GAG AGT GCT 432
 129 Gly Arg Leu Leu Ser Val Ser Glu Gln Val Phe Asn Gln Glu Ser Ala 144

55 433 AAA GTG ACA GAG CGC TTT ATC TGG GCT GGG AAT ACA ACC TCG GAG AAA 480
 145 Lys Val Thr Glu Arg Phe Ile Trp Ala Gly Asn Thr Thr Ser Glu Lys 160

60 481 GAG TAT AAC CTC TCC GGT CTG TGT ATA CGC CAC TAC GAC ACA GCG GGA 528
 161 Glu Tyr Asn Leu Ser Gly Leu Cys Ile Arg His Tyr Asp Thr Ala Gly 176

529 GTG ACC CGG TTG ATG AGT CAG TCA CTG GCG GGC GCC ATG CTA TCC CAA 576
 177 Val Thr Arg Leu Met Ser Gln Ser Leu Ala Gly Ala Met Leu Ser Gln 192

65 577 TCT CAC CAA TTG CTG GCG GAA GGG CAG GAG GCT AAC TGG AGC GGT GAC 624
 193 Ser His Gln Leu Leu Ala Glu Gly Gln Glu Ala Asn Trp Ser Gly Asp 208

	625	GAC GAA ACT GTC TGG CAG GGA ATG CTG GCA AGT GAG GTC TAT ACG ACA	672
	209	Asp Glu Thr Val Trp Gln Gly Met Leu Ala Ser Glu Val Tyr Thr Thr	224
5			
	673	CAA AGT ACC ACT AAT GCC ATC GGG GCT TTA CTG ACC CAA ACC GAT GCG	720
	225	Gln Ser Thr Thr Asn Ala Ile Gly Ala Leu Leu Thr Gln Thr Asp Ala	240
10			
	721	AAA GGC AAT ATT CAG CGT CTG GCT TAT GAC ATT GCC GGT CAG TTA AAA	763
	241	Lys Gly Asn Ile Gln Arg Leu Ala Tyr Asp Ile Ala Gly Gln Leu Lys	256
15			
	769	GGG AGT TGG TTG ACG GTG AAA GGC CAG AGT GAA CAG CTG ATT GTT AAG	816
	257	Gly Ser Trp Leu Thr Val Lys Gly Gln Ser Glu Gln Val Ile Val Lys	272
20			
	817	TCC CTG AGC TGG TCA GCC GCA GGT CAT AAA TTG CGT GAA GAG CAC GGT	864
	273	Ser Leu Ser Trp Ser Ala Ala Gly His Lys Leu Arg Glu Glu His Gly	288
25			
	865	AAC GGC GTG GTT ACG GAG TAC AGT TAT GAG CCG GAA ACT CAA CGT CTG	912
	289	Asn Gly Val Val Thr Glu Tyr Ser Tyr Glu Pro Glu Thr Gln Arg Leu	304
30			
	913	ATA GGT ATC ACC ACC CGG CGT GCC GAA GGG AGT CAA TCA GGA GCC AGA	960
	305	Ile Gly Ile Thr Thr Arg Arg Ala Glu Gly Ser Gln Ser Gly Ala Arg	320
35			
	961	GTA TTG CAG GAT CTA CGC TAT AAG TAT GAT CCG GTG GGG AAT GTT ATC	1008
	321	Val Leu Gln Asp Leu Arg Tyr Lys Tyr Asp Pro Val Gly Asn Val Ile	336
40			
	1009	AGT ATC CAT AAT GAT GCC GAA GCT ACC CGC TTT TGG CGT AAT CAG AAA	1056
	337	Ser Ile His Asn Asp Ala Glu Ala Thr Arg Phe Trp Arg Asn Gln Lys	352
45			
	1057	GTG GAG CCG GAG AAT CGC TAT GTT TAT GAT TCT CTG TAT CAG CTT ATG	1104
	353	Val Glu Pro Glu Asn Arg Tyr Val Tyr Asp Ser Leu Tyr Gln Leu Met	368
50			
	1105	AGT GCG ACA GGG CGT GAA ATG GCT AAT ATC GGT CAG CAA AGC AAC CAA	1152
	369	Ser Ala Thr Gly Arg Glu Met Ala Asn Ile Gly Gln Gln Ser Asn Gln	384
55			
	1153	CTT CCC TCA CCC GTT ATA CCT GTT CCT ACT GAC GAC AGC ACT TAT ACC	1200
	385	Leu Pro Ser Pro Val Ile Pro Val Pro Thr Asp Asp Ser Thr Tyr Thr	400
60			
	1201	AAT TAC CTT CGT ACC TAT ACT TAT GAC CGT GGC GGT AAT TTG GTT CAA	1248
	401	Asn Tyr Leu Arg Thr Tyr Thr Tyr Asp Arg Gly Gly Asn Leu Val Gln	416
65			
	1249	ATC CGA CAC AGT TCA CCC GCG ACT CAA AAT AGT TAC ACC ACA GAT ATC	1296
	417	Ile Arg His Ser Ser Pro Ala Thr Gln Asn Ser Tyr Thr Thr Asp Ile	432
70			
	1297	ACC GTT TCA AGC CGC AGT AAC CGG GCG GTA TTG AGT ACA TTA ACG ACA	1344
	433	Thr Val Ser Ser Arg Ser Asn Arg Ala Val Leu Ser Thr Leu Thr Thr	448
75			
	1345	GAT CCA ACC CGA GTG GAT GCG CTA TTT GAT TCC GGC GGT CAT CAG AAG	1392
	449	Asp Pro Thr Arg Val Asp Ala Leu Phe Asp Ser Gly Gly His Gln Lys	464
80			
	1393	ATG TTA ATA CCG GGG CAA AAT CTG GAT TGG AAT ATT CGG GGT GAA TTG	1440

	455	Met	Leu	Ile	Pro	Gly	Gln	Asn	Leu	Asp	Trp	Asn	Ile	Arg	Gly	Glu	Leu	437
5	1441	CAA	CGA	GTC	ACA	CCG	GTG	AGC	CGT	GAA	AAT	AGC	AGT	GAC	AGT	GAA	TGG	1438
	431	Gln	Arg	Val	Thr	Pro	Val	Ser	Arg	Glu	Asn	Ser	Ser	Asp	Ser	Glu	Trp	496
10	1489	TAT	CGC	TAT	AGC	AGT	GAT	GGC	ATG	CGG	CTG	CTA	AAA	GTG	AGT	GAA	CAG	1536
	497	Tyr	Arg	Tyr	Ser	Ser	Asp	Gly	Met	Arg	Leu	Leu	Lys	Val	Ser	Glu	Gln	512
15	1537	CAG	ACG	GGC	AAC	AGT	ACT	CAA	GTA	CAA	CGG	GTG	ACT	TAT	CTG	CCG	GGA	1584
	513	Gln	Thr	Gly	Asn	Ser	Thr	Gln	Val	Gln	Arg	Val	Thr	Tyr	Leu	Pro	Gly	528
20	1585	TTA	GAG	CTA	CGG	ACA	ACT	GGG	GTT	GCA	GAT	AAA	ACA	ACC	GAA	GAT	TTG	1632
	529	Leu	Glu	Leu	Arg	Thr	Thr	Gly	Val	Ala	Asp	Lys	Thr	Thr	Glu	Asp	Leu	544
25	1633	CAG	GTG	ATT	ACG	GTA	GGT	GAA	GCG	GGT	CCC	GCA	CAG	GTA	AGG	GTA	TTG	1680
	545	Gln	Val	Ile	Thr	Val	Gly	Glu	Ala	Gly	Arg	Ala	Gln	Val	Arg	Val	Leu	560
30	1681	CAC	TGG	GAA	AGT	GGT	AAG	CCG	ACA	GAT	ATT	GAC	AAC	AAT	CAG	GTG	CCG	1728
	561	His	Trp	Glu	Ser	Gly	Lys	Pro	Thr	Asp	Ile	Asp	Asn	Asn	Gln	Val	Arg	576
35	1729	TAC	AGC	TAC	GAT	AAT	CTG	CTT	GGC	TCC	AGC	CAG	CTT	GAA	CTG	GAT	AGC	1776
	577	Tyr	Ser	Tyr	Asp	Asn	Leu	Leu	Gly	Ser	Ser	Gln	Leu	Glu	Leu	Asp	Ser	592
40	1777	GAA	GGG	CAG	ATT	CTC	AGT	CAG	GAA	GAG	TAT	TAT	CCG	TAT	GGC	GGT	ACG	1824
	593	Glu	Gly	Gln	Ile	Leu	Ser	Gln	Glu	Glu	Tyr	Tyr	Pro	Tyr	Gly	Gly	Thr	608
45	1825	GCG	ATA	TGG	GCG	GCG	AGA	AAT	CAG	ACA	GAA	GCC	AGC	TAC	AAA	TTT	ATT	1872
	609	Ala	Ile	Trp	Ala	Ala	Arg	Asn	Gln	Thr	Glu	Ala	Ser	Tyr	Lys	Phe	Ile	624
50	1873	CGT	TAC	TCC	GGT	AAA	GAG	CGG	GAT	GCC	ACT	GGA	TTG	TAT	TAT	TAC	GGC	1920
	625	Arg	Tyr	Ser	Gly	Lys	Glu	Arg	Asp	Ala	Thr	Gly	Leu	Tyr	Tyr	Tyr	Gly	640
55	1921	TAC	CGT	TAT	TAT	CAA	CCT	TGG	GTG	GGT	CGA	TGG	TTG	AGT	GCT	GAT	CCG	1968
	641	Tyr	Arg	Tyr	Tyr	Gln	Pro	Trp	Val	Gly	Arg	Trp	Leu	Ser	Ala	Asp	Pro	656
60	1969	GCG	GGA	ACC	GTG	GAT	GGG	CTG	AAT	TTG	TAC	CGA	ATG	GTG	AGG	AAT	AAC	2016
	657	Ala	Gly	Thr	Val	Asp	Gly	Leu	Asn	Leu	Tyr	Arg	Met	Val	Arg	Asn	Asn	672
65	2017	CCC	ATC	ACA	TTG	ACT	GAC	CAT	GAC	GGA	TTA	GCA	CCG	TCT	CCA	AAT	AGA	2064
	673	Pro	Ile	Thr	Leu	Thr	Asp	His	Asp	Gly	Leu	Ala	Pro	Ser	Pro	Asn	Arg	688
70	2065	AAT	CGA	AAT	ACA	TTT	TGG	TTT	GCT	TCA	TTT	TTG	TTT	CGT	AAA	CCT	GAT	2112
	689	Asn	Arg	Asn	Thr	Phe	Trp	Phe	Ala	Ser	Phe	Leu	Phe	Arg	Lys	Pro	Asp	704
75	2113	GAG	GGA	ATG	TCC	GCG	TCA	ATG	AGA	CGG	GGA	CAA	AAA	ATT	GGC	AGA	GCC	2160
	705	Glu	Gly	Met	Ser	Ala	Ser	Met	Arg	Arg	Gly	Gln	Lys	Ile	Gly	Arg	Ala	720
80	2161	ATT	GCC	GCG	GGG	ATT	GCG	ATT	GCG	GGT	CTT	GCG	GCT	ACC	ATT	GCC	GCT	2208
	721	Ile	Ala	Gly	Gly	Ile	Ala	Ile	Gly	Gly	Leu	Ala	Ala	Thr	Ile	Ala	Ala	736

	2209	ACG GCT GCG GCG GCT ATC CCC GTC ATT CTG GGG GTT GCG GCC GTA GGC	2256
	737	Thr Ala Gly Ala Ala Ile Pro Val Ile Leu Gly Val Ala Ala Val Gly	752
5			
	2257	GCG GGG ATT GGC GCG TTG ATG GGA TAT AAC GTC GGT AGC CTG CTG GAA	2304
	753	Ala Gly Ile Gly Ala Leu Met Gly Tyr Asn Val Gly Ser Leu Leu Glu	769
10			
	2305	AAA GGC GGG GCA TTA CTT GCT CGA CTC GTA CAG GGG AAA TCG ACG TTA	2352
	769	Lys Gly Gly Ala Leu Leu Ala Arg Leu Val Gln Gly Lys Ser Thr Leu	784
15			
	2353	GTA CAG TCG GCG GCT GGC GCG GCT GCC GGA GCG AGT TCA GCC GCG GCT	2400
	785	Val Gln Ser Ala Ala Gly Ala Ala Ala Gly Ala Ser Ser Ala Ala Ala	800
20			
	2401	TAT GGC GCA CGG GCA CAA GGT GTC GGT GTT GCA TCA GCC GCC GGG GCG	2443
	801	Tyr Gly Ala Arg Ala Gln Gly Val Gly Val Ala Ser Ala Ala Gly Ala	816
25			
	2449	GTA ACA GCG GCT GTG GGA TCA TCG ATA AAT AAT GCT GAT CGG GGG ATT	2496
	817	Val Thr Gly Ala Val Gly Ser Trp Ile Asn Asn Ala Asp Arg Gly Ile	832
30			
	2497	GCG GCG GCT ATT GGG GCC GGG AGT GCG GTA GGC ACC ATT GAT ACT ATG	2544
	833	Gly Gly Ala Ile Gly Ala Gly Ser Ala Val Gly Thr Ile Asp Thr Met	848
35			
	2545	TTA GGG ACT GCC TCT ACC CTT ACC CAT GAA GTC GGG GCA GCG GCG GGT	2592
	849	Leu Gly Thr Ala Ser Thr Leu Thr His Glu Val Gly Ala Ala Ala Gly	864
40			
	2593	GCG GCG GCG GGT GGG ATG ATC ACC GGT ACG CAA GGG AGT ACT CGG GCA	2640
	865	Gly Ala Ala Gly Gly Met Ile Thr Gly Thr Gln Gly Ser Thr Arg Ala	880
45			
	2641	GGT ATC CAT GCC GGT ATT GCG ACC TAT TAT GGC TCC TCG ATT GGT TTT	2688
	881	Gly Ile His Ala Gly Ile Gly Thr Tyr Tyr Gly Ser Trp Ile Gly Phe	896
50			
	2689	GGT TTA GAT GTC GCT AGT AAC CCC GCC GGA CAT TTA GCG AAT TAC GCA	2736
	897	Gly Leu Asp Val Ala Ser Asn Pro Ala Gly His Leu Ala Asn Tyr Ala	912
55			
	2737	GTG GGT TAT GCC GCT GGT TTG GGT GCT GAA ATG GCT GTC AAC AGA ATA	2784
	913	Val Gly Tyr Ala Ala Gly Leu Gly Ala Glu Met Ala Val Asn Arg Ile	928
60			
	2785	ATG GGT GGT GGA TTT TTG AGT AGG CTC TTA GGC CCG GTT GTC AGC CCA	2832
	929	Met Gly Gly Gly Phe Leu Ser Arg Leu Leu Gly Arg Val Val Ser Pro	944
65			
	2833	TAT GCC GCC GGT TTA GCC AGA CAA TTA GTA CAT TTC AGT GTC GCC AGA	2880
	945	Tyr Ala Ala Gly Leu Ala Arg Gln Leu Val His Phe Ser Val Ala Arg	960
	2881	CCT GTC TTT GAG CCG ATA TTT AGT GTT CTC GGC GGG CTT GTC GGT GGT	2928
	961	Pro Val Phe Glu Pro Ile Phe Ser Val Leu Gly Gly Leu Val Gly Gly	976
	2929	ATT GGA ACT GGC CTG CAC AGA GTG ATG GGA AGA GAG AGT TCG ATT TCC	2976
	977	Ile Gly Thr Gly Leu His Arg Val Met Gly Arg Glu Ser Trp Ile Ser	992
	2977	AGA GCG TTA AGT GCT GCC GGT AGT GGT ATA GAT CAT GTC GCT GGC ATG	3024

393 Arg Ala Leu Ser Ala Ala Gly Ser Gly Ile Asp His Val Ala Gly Met 1016
 5 3025 ATT GGT AAT CAG ATC AGA GGC AGG GTC TTG ACC ACA ACC GGG ATC GCT 3071
 1009 Ile Gly Asn Gln Ile Arg Gly Arg Val Leu Thr Thr Thr Gly Ile Ala 1024
 3073 AAT GCG ATA GAC TAT GGC ACC AGT GCT GTG GGA GCC GCA CGA CGA GTT 3120
 1025 Asn Ala Ile Asp Tyr Gly Thr Ser Ala Val Gly Ala Ala Arg Arg Val 1040
 10 3121 TTT TCT TTC TAA 3132
 1041 Phe Ser Leu End 1043

15

(2) INFORMATION FOR SEQ ID NO:61

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1043 amino acids
 (B) TYPE: amino acid
 20 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61 (Tccc peptide)

1 Met Ser Pro Ser Glu Thr Thr Leu Tyr Thr Gln Thr Pro Thr Val Ser 16
 17 Val Leu Asp Asn Arg Gly Leu Ser Ile Arg Asp Ile Gly Phe His Arg 32
 30 33 Ile Val Ile Gly Gly Asp Thr Asp Thr Arg Val Thr Arg His Gln Tyr 48
 49 Asp Ala Arg Gly His Leu Asn Tyr Ser Ile Asp Pro Arg Leu Tyr Asp 64
 35 65 Ala Lys Gln Ala Asp Asn Ser Val Lys Pro Asn Phe Val Trp Gln His 80
 81 Asp Leu Ala Gly His Ala Leu Arg Thr Glu Ser Val Asp Ala Gly Arg 96
 40 97 Thr Val Ala Leu Asn Asp Ile Glu Gly Arg Ser Val Met Thr Met Asn 112
 113 Ala Thr Gly Val Arg Gln Thr Arg Arg Tyr Glu Gly Asn Thr Leu Pro 128
 129 Gly Arg Leu Leu Ser Val Ser Glu Gln Val Phe Asn Gln Glu Ser Ala 144
 45 145 Lys Val Thr Glu Arg Phe Ile Trp Ala Gly Asn Thr Thr Ser Glu Lys 160
 161 Glu Tyr Asn Leu Ser Gly Leu Cys Ile Arg His Tyr Asp Thr Ala Gly 176
 177 Val Thr Arg Leu Met Ser Gln Ser Leu Ala Gly Ala Met Leu Ser Gln 192
 50 193 Ser His Gln Leu Leu Ala Glu Gly Gln Glu Ala Asn Trp Ser Gly Asp 208
 209 Asp Glu Thr Val Trp Gln Gly Met Leu Ala Ser Glu Val Tyr Thr Thr 224
 55 225 Gln Ser Thr Thr Asn Ala Ile Gly Ala Leu Leu Thr Gln Thr Asp Ala 240
 241 Lys Gly Asn Ile Gln Arg Leu Ala Tyr Asp Ile Ala Gly Gln Leu Lys 256
 257 Gly Ser Trp Leu Thr Val Lys Gly Gln Ser Glu Gln Val Ile Val Lys 272
 60 273 Ser Leu Ser Trp Ser Ala Ala Gly His Lys Leu Arg Glu Glu His Gly 288
 289 Asn Gly Val Val Thr Glu Tyr Ser Tyr Glu Pro Glu Thr Gln Arg Leu 304
 65 305 Ile Gly Ile Thr Thr Arg Arg Ala Glu Gly Ser Gln Ser Gly Ala Arg 320

	321	Val Leu Gln Asp Leu Arg Tyr Lys Tyr Asp Pro Val Gly Asn Val Ile	355
5	337	Ser Ile His Asn Asp Ala Glu Ala Thr Arg Phe Trp Arg Asn Gln Lys	358
	353	Val Glu Pro Glu Asn Arg Tyr Val Tyr Asp Ser Leu Tyr Gln Leu Met	368
	369	Ser Ala Thr Gly Arg Glu Met Ala Asn Ile Gly Gln Gln Ser Asn Gln	384
10	385	Leu Pro Ser Pro Val Ile Pro Val Pro Thr Asp Asp Ser Thr Tyr Thr	400
	401	Asn Tyr Leu Arg Thr Tyr Thr Tyr Asp Arg Gly Gly Asn Leu Val Gln	416
15	417	Ile Arg His Ser Ser Pro Ala Thr Gln Asn Ser Tyr Thr Thr Asp Ile	432
	433	Thr Val Ser Ser Arg Ser Asn Arg Ala Val Leu Ser Thr Leu Thr Thr	443
	449	Asp Pro Thr Arg Val Asp Ala Leu Phe Asp Ser Gly Gly His Gln Lys	464
20	465	Met Leu Ile Pro Gly Gln Asn Leu Asp Trp Asn Ile Arg Gly Glu Leu	480
	481	Gln Arg Val Thr Pro Val Ser Arg Glu Asn Ser Ser Asp Ser Glu Trp	495
25	497	Tyr Arg Tyr Ser Ser Asp Gly Met Arg Leu Leu Lys Val Ser Glu Gln	512
	513	Gln Thr Gly Asn Ser Thr Gln Val Gln Arg Val Thr Tyr Leu Pro Gly	528
	529	Leu Glu Leu Arg Thr Thr Gly Val Ala Asp Lys Thr Thr Glu Asp Leu	544
30	545	Gln Val Ile Thr Val Gly Glu Ala Gly Arg Ala Gln Val Arg Val Leu	560
	561	His Trp Glu Ser Gly Lys Pro Thr Asp Ile Asp Asn Asn Gln Val Arg	576
35	577	Tyr Ser Tyr Asp Asn Leu Leu Gly Ser Ser Gln Leu Glu Leu Asp Ser	592
	593	Glu Gly Gln Ile Leu Ser Gln Glu Glu Tyr Tyr Pro Tyr Gly Gly Thr	608
	609	Ala Ile Trp Ala Ala Arg Asn Gln Thr Glu Ala Ser Tyr Lys Phe Ile	624
40	625	Arg Tyr Ser Gly Lys Glu Arg Asp Ala Thr Gly Leu Tyr Tyr Tyr Gly	640
	641	Tyr Arg Tyr Tyr Gln Pro Trp Val Gly Arg Trp Leu Ser Ala Asp Pro	656
45	657	Ala Gly Thr Val Asp Gly Leu Asn Leu Tyr Arg Met Val Arg Asn Asn	672
	673	Pro Ile Thr Leu Thr Asp His Asp Gly Leu Ala Pro Ser Pro Asn Arg	688
	689	Asn Arg Asn Thr Phe Trp Phe Ala Ser Phe Leu Phe Arg Lys Pro Asp	704
50	705	Glu Gly Met Ser Ala Ser Met Arg Arg Gly Gln Lys Ile Gly Arg Ala	720
	721	Ile Ala Gly Gly Ile Ala Ile Gly Gly Leu Ala Ala Thr Ile Ala Ala	736
55	737	Thr Ala Gly Ala Ala Ile Pro Val Ile Leu Gly Val Ala Ala Val Gly	752
	753	Ala Gly Ile Gly Ala Leu Met Gly Tyr Asn Val Gly Ser Leu Leu Glu	768
	769	Lys Gly Gly Ala Leu Leu Ala Arg Leu Val Gln Gly Lys Ser Thr Leu	784
60	785	Val Gln Ser Ala Ala Gly Ala Ala Ala Gly Ala Ser Ser Ala Ala Ala	800
	801	Tyr Gly Ala Arg Ala Gln Gly Val Gly Val Ala Ser Ala Ala Gly Ala	816
65	817	Val Thr Gly Ala Val Gly Ser Trp Ile Asn Asn Ala Asp Arg Gly Ile	832
	833	Gly Gly Ala Ile Gly Ala Gly Ser Ala Val Gly Thr Ile Asp Thr Met	848

5 849 Leu Gly Thr Ala Ser Thr Leu Thr His Glu Val Gly Ala Ala Ala Gly 864
965 Gly Ala Ala Gly Gly Met Ile Thr Gly Thr Gln Gly Ser Thr Arg Ala 880
381 Gly Ile His Ala Gly Ile Gly Thr Tyr Tyr Gly Ser Trp Ile Gly Phe 896
397 Gly Leu Asp Val Ala Ser Asn Pro Ala Gly His Leu Ala Asn Tyr Ala 912
10 913 Val Gly Tyr Ala Ala Gly Leu Gly Ala Glu Met Ala Val Asn Arg Ile 928
929 Met Gly Gly Gly Phe Leu Ser Arg Leu Leu Gly Arg Val Val Ser Pro 944
15 945 Tyr Ala Ala Gly Leu Ala Arg Gln Leu Val His Phe Ser Val Ala Arg 960
961 Pro Val Phe Glu Pro Ile Phe Ser Val Leu Gly Gly Leu Val Gly Gly 976
977 Ile Gly Thr Gly Leu His Arg Val Met Gly Arg Glu Ser Trp Ile Ser 992
20 993 Arg Ala Leu Ser Ala Ala Gly Ser Gly Ile Asp His Val Ala Gly Met 1008
1009 Ile Gly Asn Gln Ile Arg Gly Arg Val Leu Thr Thr Thr Gly Ile Ala 1024
25 1025 Asn Ala Ile Asp Tyr Gly Thr Ser Ala Val Gly Ala Ala Arg Arg Val 1040
1041 Phe Ser Leu 1043

30

We claim:

1. A composition, comprising an effective amount of a
5 *Photorhabdus* protein toxin that has functional activity against
an insect.

2. The composition of Claim 1, wherein the *Photorhabdus*
toxin is produced by a purified culture of *Photorhabdus*, a
transgenic plant, Baculovirus, or heterologous microbial host.
10

3. The composition of Claim 2, wherein the *Photorhabdus*
toxin produced by a purified culture of *Photorhabdus luminescens*.

4. The composition of Claim 2, wherein the toxin is
15 produced from a purified culture of *Photorhabdus luminescens*
strain designated ATCC 55397.

5. The composition of Claim 2, wherein the toxin is
produced by a purified culture of *Photorhabdus luminescens* strain
20 designated W-14.

6. The composition of Claim 1, wherein the toxin is
produced by a purified culture of *Photorhabdus* strain designated
WX-1, WX-2, WX-3, WX-4, WX-5, WX6, WX-7, WX-8, WX-9, WX-10, WX-
25 11, WX-12, WX-14, WX-15, H9, Hb, Hm, HP88, NC-1, W30, WIR, ATCC#
43948, ATCC# 43949, ATCC# 43950, ATCC# 43951, or ATCC# 43952.

7. The composition of Claim 2, wherein the toxin is
produced from a purified culture of *Photorhabdus luminescens*
30 strain designated WX-1, WX-2, WX-3, WX-4, WX-5, WX-6, WX-7, WX-8,
WX-9, WX-10, WX-11, WX-12, WX-14, WX-15, H9, Hb, Hm, HP88, NC-1,
W30, WIR, ATCC# 43948, ATCC# 43949, ATCC# 43950, ATCC# 43951, or
ATCC# 43952.

8. The composition of Claim 1, wherein the toxin is
35 respresented by amino acid sequence is SEQ ID NO:12.

9. The composition of Claim 6, wherein the composition is a
mixture of one or more toxins produced from purified cultures of
40 *Photorhabdus*.

10. The composition of Claim 1 or 6, wherein the insect is of the order *Lepidoptera*, *Coleoptera*, *Hymenoptera*, *Diptera*, *Dictyoptera*, *Acarina* or *Homoptera*.

5

11. The composition of Claim 1 or 6, wherein the insect species is from order *Coleoptera* and is Southern Corn Rootworm, Western Corn Rootworm, Colorado Potato Beetle, Mealworm, Boll Weevil or Turf Grub.

10

12. The composition of Claim 1 or 6, wherein the insect species is from order *Lepidoptera* and is Beet Armyworm, Black Cutworm, Cabbage Looper, Codling Moth, Corn Earworm, European Corn Borer, Tobacco Hornworm, or Tobacco Budworm.

15

13. The composition of Claim 1 or 6, wherein the toxin is formulated as a sprayable insecticide.

14. The composition of Claim 1 or Claim 6, wherein the toxin is formulated as a bait matrix and delivered in an above ground or below ground bait station.

20

15. A method of controlling an insect, comprising orally delivering to an insect an effective amount of a protein toxin that has functional activity against an insect, wherein the protein is produced by a purified bacterial culture of the genus *Photobacterium*.

25

16. The method of Claim 15, wherein the bacterium is a purified culture of *Photobacterium luminescens*.

30

17. The method of Claim 15, wherein the toxin is produced from a purified culture of *Photobacterium luminescens* strain designated ATCC 55397.

35

18. The method of Claim 16, wherein the toxin is produced from a purified culture of *Photobacterium luminescens* strain designated W-14.

19. The method of Claim 15, wherein the toxin is produced from a purified culture of *Photobhabdus* strains designated WX-1, WX-2, WX-3, WX-4, WX-5, WX-6, WX-7, WX-8, WX-9, WX-10, WX-11, WX-12, WX-14, WX-15, H9, Hb, Hm, HP88, NC-1, W30, WIR, ATCC# 43948, ATCC# 43949, ATCC# ATCC# 43950, ATCC# 43951, or ATCC# 43952.

20. The method of Claim 15, wherein the toxin is produced from a purified culture of *Photobhabdus luminescens* strains designated WX-1, WX-2, WX-3, WX-4, WX-5, WX-6, WX-7, WX-8, WX-9, WX-10, WX-11, WX-12, WX-14, WX-15, H9, Hb, Hm, HP88, NC-1, W30, WIR, ATCC# 43948, ATCC# 43949, ATCC# ATCC# 43950, ATCC# 43951, or ATCC# 43952.

21. The method of Claim 19, wherein a mixture of one or more toxins is produced from a purified culture of *Photobhabdus* and said toxins are orally delivered to an insect.

22. The method of Claim 15, wherein the toxin is produced by a prokaryotic host transformed with a gene encoding the toxin.

23. The method of Claim 15, wherein the toxin is produced by a eukaryotic host transformed with a gene encoding the toxin.

24. The method of Claim 23, wherein the eukaryotic host is baculovirus.

25. The method of Claim 15 or 19, wherein the insect is of the order *Lepidoptera*, *Coleoptera*, *Hymenoptera*, *Diptera*, *Dictyoptera*, *Acarina* or *Homoptera*.

26. The method of Claim 15 or 19, wherein the insect species is from order *Coleoptera* and is Southern Corn Rootworm, Western Corn Rootworm, Colorado Potato Beetle, Mealworm, Boll Weevil or Turf Grub.

27. The method of Claim 15 or 19, wherein the insect species is from order *Lepidoptera* and is Beet Armyworm, Black Cutworm, Cabbage Looper, Codling Moth, Corn Earworm, European Corn Borer, Tobacco Hornworm, or Tobacco Budworm.

28. The method of Claim 15 or 19, wherein the toxin is formulated as a sprayable insecticide.

29. The method of Claim 15 or Claim 19, wherein the toxin is formulated as a bait matrix and delivered in an above ground or below ground bait station.

30. A method of isolating a gene coding for a protein subunit, comprising the steps of: constructing at least one RNA or DNA oligonucleotide molecule that corresponds to at least a part of a DNA coding region of an amino acid sequence selected from a group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO: 13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, and SEQ ID NO:43, wherein the nucleotide molecule is used to isolate genetic material from *Photobacterium* or *Photobacterium luminescens*.

31. A method for expressing a protein produced by a purified bacterial culture of the genus *Photobacterium* in a prokaryotic or eukaryotic host in an effective amount so that the protein has functional activity against an insect, wherein the method comprises: constructing a chimeric DNA construct having 5' to 3' a promoter, a DNA sequence encoding a protein, a transcription terminator, and then transferring the chimeric DNA construct into the host.

32. The method of Claim 31, wherein the protein has functional activity against insects selected from a group consisting of *Coleoptera*, *Lepidoptera*, *Diptera*, *Homoptera*, *Hymenoptera*, *Dictyoptera*, and *Acarina*.

33. The method of Claim 31, wherein the protein encoded by the DNA sequence has an N-terminal amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:14, SEQ

ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19,
SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID
NO:24, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41,
SEQ ID NO:42, and SEQ ID NO:43.

5

34. The method of Claim 31, wherein the protein encoded by
the DNA sequence includes the amino acid sequence selected from
the group consisting of SEQ ID NO:12, SEQ ID NO:26, SEQ ID NO:28,
SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:35, SEQ ID
10 NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55,
SEQ ID NO:57, SEQ ID NO:59 and SEQ ID NO:61.

35. A chimeric DNA construct, adapted for expression in a
prokaryotic or eukaryotic host comprising, 5' to 3' a
15 transcriptional promoter active in the host; a DNA sequence
encoding a *Photobacterium* protein that has functional activity
against an insect; and a transcriptional terminator.

36. A chimeric DNA construct of Claim 35, wherein the
20 protein encoded by the DNA sequence has an N-terminal amino acid
sequence selected from the group consisting of SEQ ID NO:1, SEQ
ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ
ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO: 13,
SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID
25 NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22,
SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:38, SEQ ID NO:39, SEQ ID
NO:40, SEQ ID NO:41, SEQ ID NO:42, and SEQ ID NO:43.

37. The chimeric DNA construct of Claim 35, wherein the
30 protein encoded by the DNA sequence has an amino acid sequence
selected from the group consisting of SEQ ID NO:12, SEQ ID NO:26,
SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID
NO:35, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53,
SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:61.

35

38. The chimeric DNA construct of Claim 35, wherein the DNA
sequence encoding the *Photobacterium luminescens* protein is
selected from the group comprising SEQ ID NO:11, SEQ ID NO:25,
SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID

NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54,
SEQ ID NO:56, SEQ ID NO: 58, and SEQ ID NO:60.

39. The chimeric DNA construct of Claim 35, wherein the
5 host is baculovirus.

40. An isolated and substantially purified preparation
comprising, a DNA molecule capable of encoding an effective
amount of a protein that is produced by a bacterium of the genus
10 *Photorhabdus* and that has functional activity against an insect.

41. The preparation of Claim 40, wherein the bacterium is
Photorhabdus luminescens.

15 42. A purified preparation comprising, a protein produced
by *Photorhabdus* or *Photorhabdus luminescens* having an N-terminal
amino acid sequence selected from the group consisting of SEQ ID
NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID
NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID
20 NO: 13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17,
SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID
NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:38, SEQ ID NO:39,
SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, and SEQ ID NO:43.

25 43. A purified protein preparation comprising, a protein
that has an N-terminal amino acid sequence selected from the
group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID
NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID
NO:9, and SEQ ID NO:10, SEQ ID NO: 13, SEQ ID NO:14, SEQ ID NO:15,
30 SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID
NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24,
SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID
NO:42, and SEQ ID NO:43.

35 44. A purified protein preparation comprising, a protein
selected from the group of SEQ ID NO:12, SEQ ID NO:26, SEQ ID
NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:35,
SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID
NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:61.

40

45. A purified DNA preparation comprising, a DNA sequence selected from the group consisting of SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54,
5 SEQ ID NO:56, SEQ ID NO:58 and SEQ ID NO:60, wherein the DNA sequence is isolated from its native host.

46. A purified protein preparation comprising, a *Photorhabdus luminescens* protein with at least one subunit having
10 an approximate molecular weight between 18 kDa to about 230 kDa; between about 160 kDa to about 230 kDa; 100 kDa to 160 kDa; about 80 kDa to about 100 kDa; or about 50 kDa to about 80 kDa.

47. A purified protein preparation comprising, a *Photorhabdus luminescens* protein with at least one subunit having
15 an approximate molecular weight of about 280 kDa.

48. A substantially pure microorganism culture comprising, ATCC 55397.
20

49. The culture of Claim 48, wherein the culture is a derivative of ATCC 55397 that produces a protein toxin that has functional activity against an insect.

25 50. A substantially pure microorganism culture comprising, H9.

51. A substantially pure microorganism culture comprising, Hb.
30

52. A substantially pure microorganism culture comprising, Hm.

53. A substantially pure microorganism culture comprising, HP88.
35

54. A substantially pure microorganism culture comprising, NC-1.

40 55. A substantially pure microorganism culture comprising,

W30.

56. A substantially pure microorganism culture comprising,
WIR.

5

57. A transgenic plant comprising in its genome, a chimeric artificial gene construction imbuing the plant with an ability to express an effective amount of a *Photorhabdus* protein that has functional activity against an insect.

10

58. The transgenic plant of Claim 57, wherein the plant is transformed using acceleration of genetic material coated onto microparticles directly into cells, *Agrobacteria*, whiskers, or electroporation techniques

15

59. The transgenic plant of Claim 57, wherein the selectable marker is selected from the group consisting of kanamycin, neomycin, glyphosate, hygromycin, methotrexate, phosphinothricin (bialophos), chlorosulfuron, bromoxynil, dalapon and the like.

20

60. The transgenic plant of Claim 57, wherein the promoter is selected from the group consisting of octopine synthase, nopaline synthase, mannopine synthase, 35S, 19S, ribulose-1,6-bisphosphate (RUBP) carboxylase small subunit (ssu), beta-conglycinin, phaseolin, alcohol dehydrogenase (ADH), heat-shock, ubiquitin, zein, oleosin, napin, or acyl carrier protein (ACP).

25

61. The transgenic plant of Claim 57, wherein embryogenic tissue, callus tissue type I or II, hypocotyl, meristem, or plant tissue during dedifferentiation is used in preparing the transgenic plant.

30

62. The transgenic plant of Claim 57, wherein the chimeric gene is a DNA sequence which encodes a *Photorhabdus* protein that has functional activity against an insect and at least one codon of the gene has been modified so that the codon is a plant preferred codon.

35

63. A method of controlling an insect comprising orally delivering to an insect an effective amount of a protein toxin, wherein the protein is produced by a transgenic plant, which said insect feeds.

5

64. A composition of matter, comprising a purified DNA sequence from a purified bacterial culture from the genus *Photorhabdus*.

1 ATG CAG GAT TGT COG GAA GTA TOG ATT ACA ACG CTG TCA CTT COC AAA GGT GGC GGT
TAC GTC CTA ACA GGC CTT CAT AGC TAA TGT TGC GAC AGT GAA GGG TTT OCA COG OCA
10 Met Gln Asp Cys Pro Glu Val Ser Ile Thr Thr Leu Ser Leu Pro Lys Gly Gly Gly
P2Psh
58 GCT ATC AAT GGC ATG GGA GAA GCA CTG AAT GCT GGC OCT GAT GGA ATG GGC TOC
CGA TAG TTA CCG TAC OCT CTT CGT GAC TTA CGA CTA OCT TAC TAC CCG AGG
20 Ala Ile Asn Gly Met Gly Glu Ala Leu Asn Ala Ala Gly Pro Asp Gly Met Ala Ser
115 CTA TCT CTG CCA TTA OOC CTT TOG AOC GGC AGA GGG ACG GCT CCT GGA TTA TOG CTG
GAT AGA GAC GGT AAT GGG GAA AGC TGG CCG TCT OOC TGC CGA GGA OCT AAT AGC GAC
39 Leu Ser Leu Pro Leu Pro Leu Ser Thr Gly Arg Gly Thr Ala Pro Gly Leu Ser Leu
172 ATT TAC AGC AAC AGT GCA GGT AAT GGG OCT TTC GGC ATC GGC TGG CAA TGC GGT GTT
TAA ATG TCG TTG TCA OGT OCA TTA OOC GGA AAG OCG TAG CCG ACC GTT ACG CCA CAA
58 Ile Tyr Ser Asn Ser Ala Gly Asn Gly Pro Phe Gly Ile Gly Trp Gln Cys Gly Val
229 ATG TOC ATT AGC CGA OGC ACC CAA CAT GGC CTT CAA CAT TGA CGA OGT
TAC AGG TAA TCG GCT GCG TGG GTT GTA CCG GAA GTT GTA ACT GCT GCA
77 Met Ser Ile Ser Arg Arg Thr Gln His Gly Leu Gln His ... Arg Arg
P2.3.5R

FIG. 1

2/8

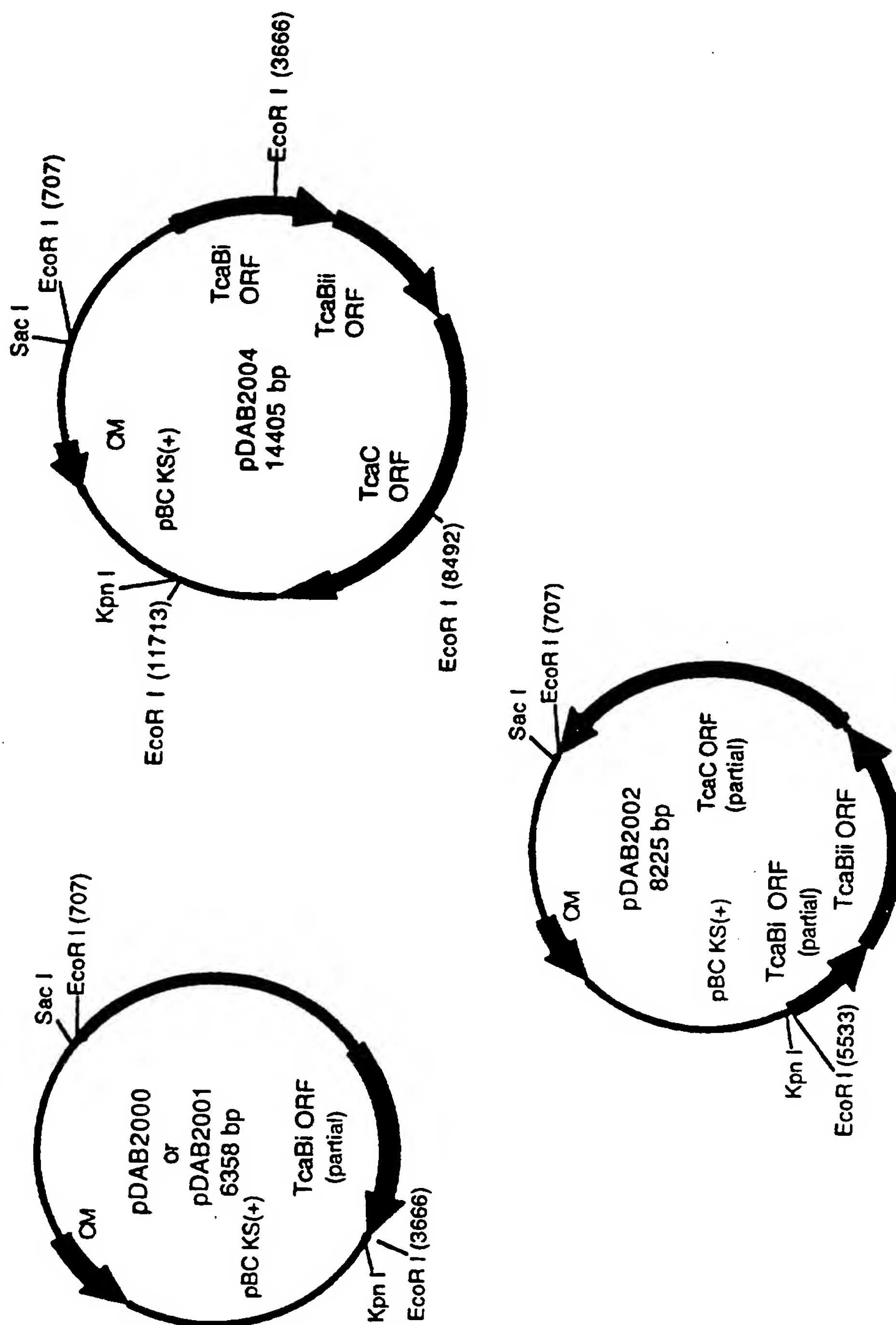


FIG. 2

3 / 8

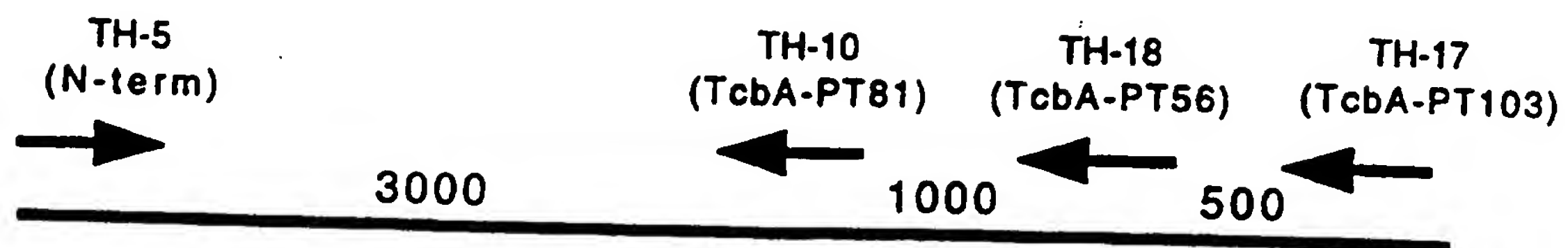


FIG. 3

TcbA	1740	1750	1760	1770	1780
	SSAQALKNDS	EPMDFSGANA	LYFWELFYTT	PMMTAHRLLO	EQNFDAAANHW
TcaBi	gS	nPvDFSGpyg	iYlWEiFfhi	PflvtvRmgt	EQryedAdtW>
	^^	^^^^^^^^^v	^^^^^^^^^^	^~^~^v^~v	^^~^~^~v^
TcbA	1790	1800	1810	1820	1830
	FRYVWSPSGY	IVDGKIAIYH	WNVRLPLEEDT	SWNAQQLDST	DPDAVAQDDP
TcaBi	rdangql				
	490	510	520	530	
	ykyifrsagY	ImDGskprY-	WNVmPLqldT	aWdttQpatT	DPDviAmaDP>
	^^^^~^~^~	^^^^~v^v	^^~^~^v^~	^^^^v^v~^	^^~^~^v~^
TcbA	1840	1850	1860	1870	1880
	MHYKVATFMA	TLDLLMARGD	AAYRQLERDT	LAEAKMWYTQ	ALNLLGDEPO
TcaBi	540	550	560	570	580
	MHYKlAiFlh	TLDLLiARGD	sAYRQLERDT	LvEAKMyYiQ	AqqLLGprPd>
	^^^^~^~v	^^^^^^^^^^	^^^^^^^^^^	^~^~^~^~^	^v^~^~^v^
TcbA	1890	1900	1910	1920	1930
	VMLSTTWANP	TLGNAASKTT	QQVRQOVLTO	LRLNSRVKTP	LLGTANSLTA
TcaBi	600				
	ihhtnTWpNP	TLsk>			
	^v^~^~^~	^^^^			
TcbA	1940	1950	1960	1970	1980
	LFLPQENSKL	KGYWRTLAQR	MFNLRHNLIS	DGQPLSLPLY	AKPADPKALL
TcaBii	20	30	40	50	60
	_FLPpyNdVL	lGYWdkLeIR	lyNLRHNLIS	DGQPLnLPLY	AtPvDPKtLq>
	^^~^v~^v	v^~^v~^v	^^^^^^^^^^	^^^^^^^^^^	^^~^~^~v
TcbA	1990	2000	2010	2020	2030
	SAAVSASQGG	ADLPKAPLTI	HRFPOMLEGA	RGLVNQLIQF	GSSLLGYSER
TcaBii	70	80	90	100	110
	rqqaggdgtG	sspaggqgsV	qRyPlLvErA	RsaVslltQF	GnSLqtltlEh>
	-----v~^	^~^v^~^v	^^^^v^~^v	^^v^~^v~^	^^^^v~^v
TcbA	2040	2050	2060	2070	2080
	QDAEAMSQLL	QTQASELILT	SIRMQDNQLA	ELDSEKTALQ	VSLAGVQQRf
TcaBii	120	130	140	150	160
	QDnEkMtill	QTQqeailkh	qhdiQqNnLk	gLqhs1TALQ	aSrdGdtlRq>
	^^~^v^~^	^^~^~^~v	v^v^~^~^v	^^~^v~^~	^~^v~^v^v

FIG. 4A

FIG. 4B

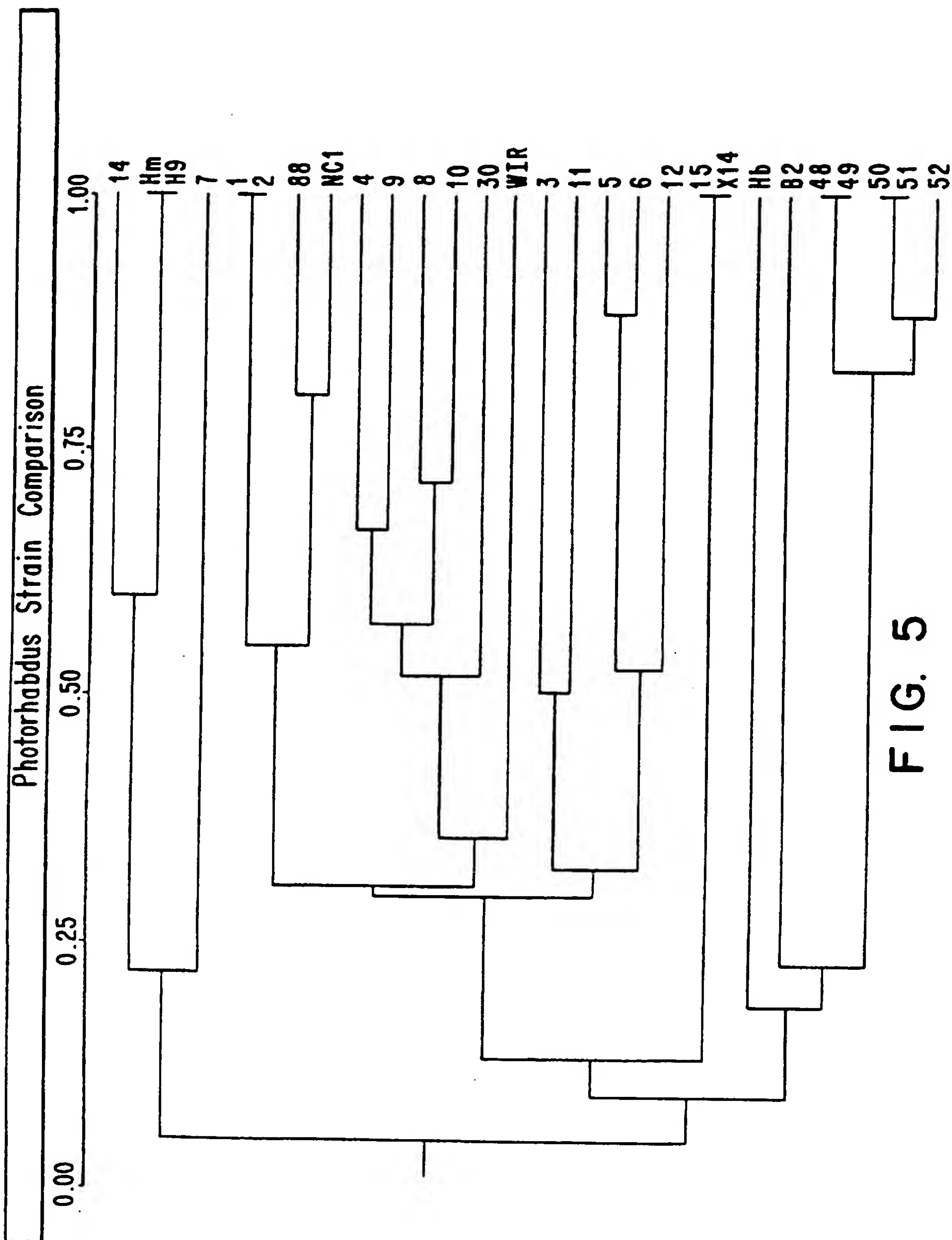


FIG. 5

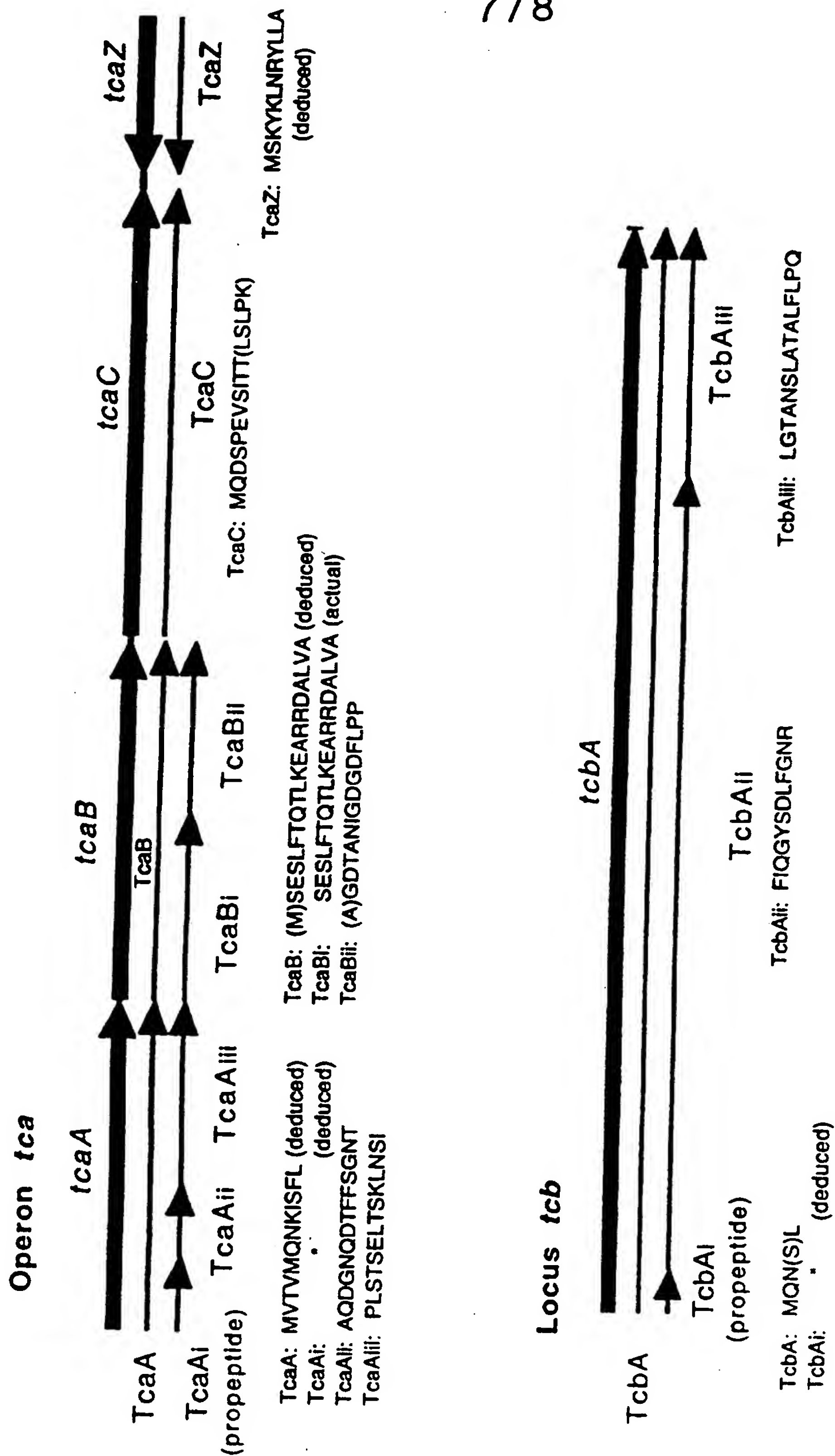


FIG. 6A

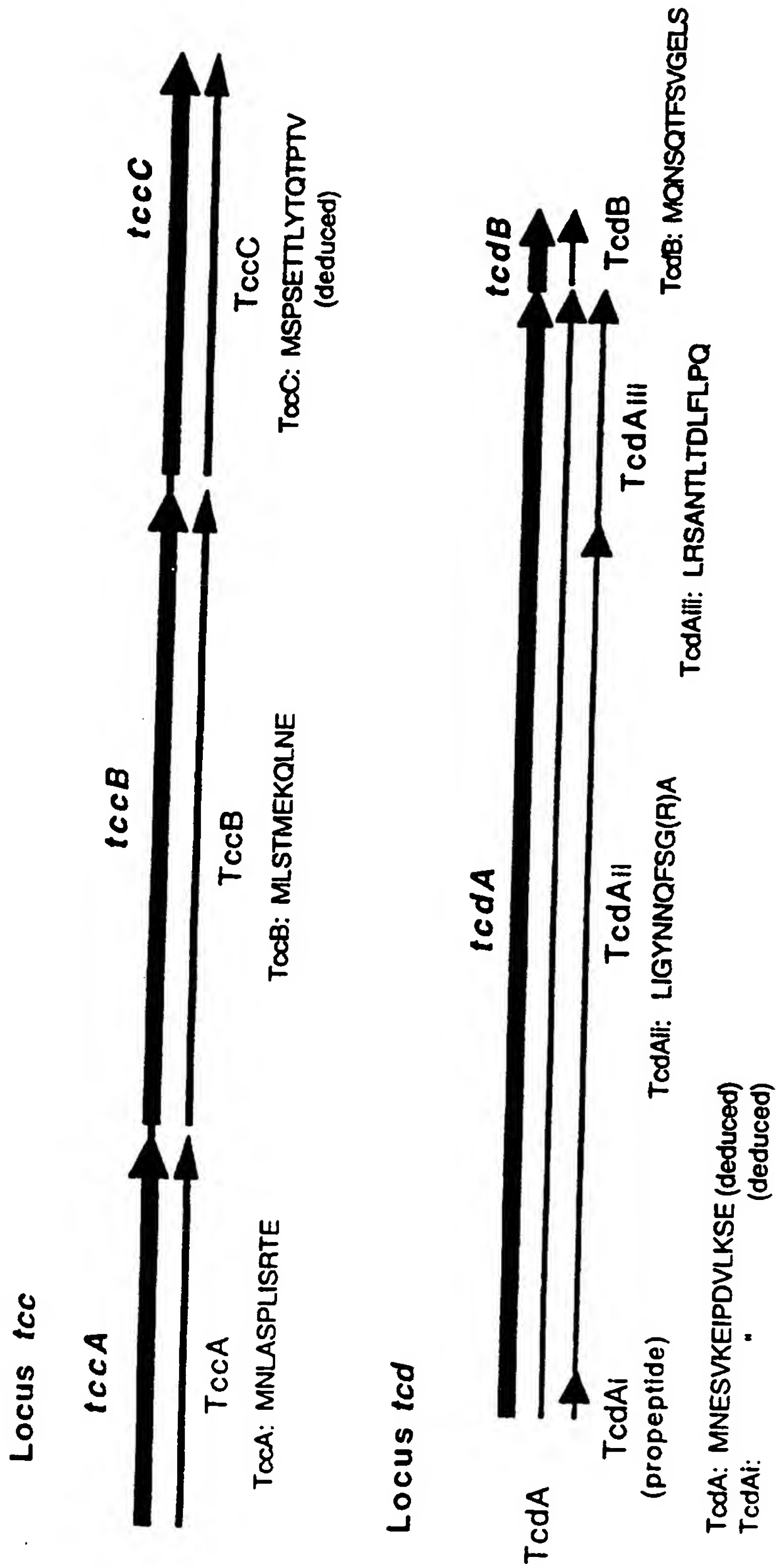


FIG. 6B

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US96/18003

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : 536/23.7, 24.1; 435/172.3, 240.4, 320.1; 800/205; 47/58

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.7, 24.1; 435/172.3, 240.4, 320.1; 800/205; 47/58

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, CABA, CAPLUS, MEDLINE, GENBANK, BIOSIS

search terms: photorhabdus, xenorhabdus, luminescens, insecticide, nematode, lepidoptera

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	CLARKE et al. Virulence Mechanisms of <i>Photorhabdus</i> sp. Strain K122 toward Wax Moth Larvae. Journal of Invertebrate Pathology. 1995, Vol. 66, pages 149-155, see entire document.	1-64
Y	US 5,039,523 A (PAYNE ET AL.) 13 August 1991, columns 1-10.	1-64
Y	US 5,254,799 A (DE GREVE ET AL.) 19 October 1993, columns 1-14.	1-64



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	* T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
* A		document defining the general state of the art which is not considered to be of particular relevance
* E		earlier document published on or after the international filing date
* L		document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
* O		document referring to an oral disclosure, use, exhibition or other means
* P		document published prior to the international filing date but later than the priority date claimed
	* X	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
	* Y	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
	* A	document member of the same patent family

Date of the actual completion of the international search

23 DECEMBER 1996

Date of mailing of the international search report

28 JAN 1997

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

THOMAS HAAS

Telephone No. (703) 305-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/18003

A. CLASSIFICATION OF SUBJECT MATTER: IPC (6):

C12N 5/14, 15/00, 15/05, 15/09, 15/29, 15/31, 15/64, 15/82; A01G 13/00; A01H 1/00